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**SURROGATE CELL GENE EXPRESSION SIGNATURES FOR EVALUATING  
THE PHYSICAL STATE OF A SUBJECT**

This application claims priority from U.S. Provisional Patent Application No. 60/473,089, filed May 23, 2003, which is herein incorporated by reference in its entirety.

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**FIELD OF THE INVENTION**

15 The present invention relates to non-invasive and minimally invasive techniques for evaluating the physical state of a subject, including diagnosing a disease, disorder, or physical state of the subject, determining the prognosis of the subject, determining a subject's susceptibility for a disease, disorder, or physical state and determining, developing and monitoring treatment for the same. The invention also relates to identifying  
20 genetic alterations contributing to, or susceptibility for, development of a disease, disorder, or physical state, and for diagnosis, prognosis and treatment of the disease, disorder, or physical state.

**BACKGROUND OF THE INVENTION**

25 Although cancer mortality rates have decreased over the past decade, through pre-symptomatic screening programs and major improvements in cancer treatment, survival rates are still low in patients presenting with a more advanced stage cancer at the time of diagnosis. Thus, effective management of any cancer relies heavily on an early diagnosis, coupled with a need to obtain accurate information on the classification and stage of the

cancer itself, and thus limitations of traditional diagnostic and prognostic techniques may currently hinder the management of cancer.

Current techniques for the screening and risk assessment of chronic disease states in general, and cancer in particular, are frequently based upon the measurement of either individual serum biomarkers, or expression of individual genes in circulating cells, such as disseminated tumor cells. In disease states for which such non-invasive tests are available they usually comprise a prerequisite to more invasive, surgical biopsy procedures.

Examples of serum biomarkers used in the clinical diagnosis of cancer include CA 125 (ovarian cancer), CA 15-3 and CA 27-29 (breast cancer), carcinoembryonic antigen, CEA (ovarian, lung, breast, pancreas, and gastrointestinal tract cancers), prostate specific antigen, PSA (prostate cancer), alpha fetoprotein, AFP (primary liver cancer or germ cell cancer), human chorionic gonadotropin, HCG (choriocarcinoma, cancers of the testis, ovary, liver, stomach, pancreas, and lung) CA 19-9 (colorectal cancer pancreatic, stomach, and bile duct cancer) neuron-specific enolase, NSE (neuroblastoma; small cell lung cancer; Wilms' tumor; melanoma; and cancers of the thyroid, kidney, testicle, and pancreas (Source: National Cancer Institute, on the Worldwide Web at [nci.nih.gov](http://nci.nih.gov))

Diagnosis of psychiatric and neurological diseases for which the molecular etiology is largely unknown, such as schizophrenia or not too well understood such as in Alzheimer's disease, still depend mainly on behavioral evaluation of patients, and no clinically proven, blood-based, tests are available to date. Individual circulating biomarkers, however, are beginning to be discovered. In Alzheimer's disease, for instance, a serum elevation of the iron transporter p97 (Kim DK, *et al.* Neuropsychopharmacology 2001;25(1):84-90) or an increase in antibody-mediated brain to plasma amyloid-beta efflux (DeMattos RB, *et al.*, Science 2002, 295:2264-2267) have been described. Furthermore, Ilani *et al.* have shown an increased level of D3 dopamine receptor mRNA in circulating blood lymphocytes in individuals with schizophrenia (Ilani *et al.* Proc Natl Acad Sci U S A 2001;98(2):625-8).

For cancer, diagnostic tests based on single circulating biomarkers possess a number of limitations, including lack of specificity and sensitivity in the diagnosis and, also a lack of prognostic information. This ultimately yields high numbers of false positive diagnoses,

and consequently unnecessarily large numbers of surgical biopsies. Alternatively, in a significant number of patients malignancies evade detection due to the inherent rate of false negative test results.

- There is growing evidence that individuals with a malignant disease such as breast cancer or prostate cancer, exhibit immune responses that can be detected at the level of altered gene expression in leukocytes circulating in peripheral blood. Quantitation of the mRNA transcripts in leukocytes of a number of individual genes has demonstrated associations between gene expression levels and the presence of a tumor in patients with breast and prostate cancer.
- 10 The recent development of microarray technology has permitted simultaneous measurement of the expression levels of thousands of genes, and also allowed a comparison of multiple data sets between multiple experiments. Investigators have begun to employ this technology, based upon sample cDNA probe hybridization to DNA-based microarrays, to identify and isolate genes differentially expressed among many tissues and cell lines.
- 15 Microarray technology will become a global gene expression diagnostic tool (Cole *et al.*, Nat Genet. 1999; 21(1 Suppl):38-41.; Howell SB, Mol Urol. 1999; 3(3):295-300). Already, breakthrough experiments have shown that molecular profiles, or gene expression signatures, can be deduced from microarray expression analysis of tumor samples. Researchers have used statistical algorithms to compare individual expression signatures, and then employed these comparisons to distinguish between forms of myeloid leukemia
- 20 (Golub *et al.*, Science 1999; 286(5439):531-7), and B-cell lymphoma (Alizadeh *et al.*, Nature 2000; 403(6769):503-11). Furthermore, analysis of tumor tissue from individual patients has permitted identification of both stages and individual classes of breast cancer (Perou *et al.*, Nature 2000; 406(6797):747-52), malignant melanoma (Bittner *et al.*, Nature
- 25 2000; 406(6795):536-40), and prostate cancer (Dhanasekaran *et al.*, Nature 2001; 412(6849):822-6; Luo *et al.*, Mol Carcinog 2002; 33(1):25-35). Additionally, utilizing microarray technology van't Veer *et al.*, have shown that the clinical status and clinical outcome of breast cancer can be predicted by gene expression analysis of tumor tissue (Nature 2002 ;415(6871):530-6).

Even at this early stage in the clinical development of this technology, it is becoming clear that microarray analysis will be able to provide important diagnostic and prognostic information for many tumor types. However, although these investigations of solid tumors provide detailed information on the pathology and malignant process of the tumor, invasive surgery or biopsy is always necessary to obtain the tumor tissue studied, and although investigations are underway to determine the feasibility of minimally traumatic biopsy sampling procedures for obtaining tissue for microarray analysis, a current report documents problems such as very low yields of extracted RNA (Assersohn *et al.*, Clin Cancer Res. 2002; 8(3):794-801).

A link between cancer and altered gene expression in the immune system has been previously documented. Tumor-induced immunosuppression allows malignant cells to evade the immune system, and some tumors are commonly found in individuals with compromised immune function. For example, Kaposi's sarcoma has become a very common and highly aggressive neoplastic complication of AIDS (Ensoli & Sirianni, Crit Rev Oncog 1998; 9(2):107-24), and it has been proposed that chronic inflammation, resulting from infective and/or non-infective agents, may provide the ideal environment for the cellular development of cancer (O'Byrne & Dagleish, Br J Cancer 2001;85(4):473-83).

Many mechanisms are thought to be involved in the altered immune response of cancer patients. These include decreased natural killer (NK) cell cytotoxicity (Kono *et al.*, Clin Cancer Res. 1996; 2(11):1825-8.), the production in the tumor of cytokines and growth factors that have known suppressive effects on leukocyte function (*e.g.* interleukin 6 (IL-6), IL-4 and TGF-beta1), (Oliver and Nouri, Cancer Surv. 1992; 173-204), and defective cytokine release from T-cells, such as a decrease in IL-2 (Lopez *et al.*, Cell Immunol. 1998; 190(2):141-55).

Research to further elucidate the immune responses observed in cancer patients has mainly focused on measuring the level of genes or protein products from cells within the microenvironment of the tumor, such as IL-2 mRNA transcript levels in tumor infiltrating lymphocytes within primary human breast carcinomas (Lopez *et al.*, 1998) and adenocarcinomas of the prostate (Elsasser-Beile *et al.*, J. Cancer Res Clin Oncol. 1993; 119(7):430-3). However, a number of groups have also reported altered levels of the



mRNA and/or protein products of individual genes in leukocyte cells within the circulating peripheral blood of cancer patients.

Veltri and colleagues have reported that IL-8 mRNA expression is up-regulated in patients with metastatic prostate cancer relative to control subjects (Veltri *et al.*, Urology 1999; 53(1):139-47). Specifically, these investigators carried out an analysis of IL-8 mRNA levels in peripheral blood from metastatic patients and normal control subjects (pooled into one sample), employing IL-8 gene specific primers for RT-PCR experiments, and 25 cycles of amplification in the PCR. The results documented the presence of IL-8 products in all metastatic prostate cancer patient samples, while in the pool of control samples no amplification of IL-8 was observed (Veltri *et al.*, 1999). As discussed below, the present inventors have performed similar experiments to seek to confirm these results.

Recently, a study was initiated to investigate expression levels of the mismatch repair genes, MSH2 and MLH1 in prostate cancer (Strom *et al.*, Prostate 2001; 1;47(4):269-75). Strom *et al.*, performed RT-PCR analysis of leukocyte samples from 70 prostate cancer subjects (metastatic patients were excluded from this study), and 97 matched controls. Their results implied that although considerable variation occurred among patients, the mean expression levels for both genes were significantly lower in the patients than controls. Although the authors conclude that decreased expression of MLH1 is a risk factor for prostate cancer, they also state that the decreased expression of both genes may be caused by disease status, a conclusion that is consistent with this hypothesis. The present invention provides preliminary data that reproduces these results. Veltri *et al.*, further reported that increasing concentrations of serum IL-8 protein could be positively correlated with increasing tumor burden, and that serum IL-8 levels correctly distinguished among patients classified to one of four known stages of prostate cancer (Veltri *et al.*, 1999). Additionally, the authors reported unpublished data showing that quantitative RT-PCR analysis of IL-6 and IL-10 mRNA levels also yielded a marked difference between prostate cancer patients and control subjects, and these results have been published by Ralph *et al.*, (US Patent No. 6,190,857). Earlier studies that have measured serum levels of IL-6 and IL-10 proteins in cancer patients support these observations. Specifically, IL-6 serum levels have been shown to provide prognostic information on prostate tumors (Nakashima *et al.*, Cancer Res. 2000; 6(7):2702-6), and serum IL-10 levels have been

correlated with the presence of a prostate tumor (Filella *et al.*, Prostate 2000; 44(4):271-4). A decrease in IL-10 serum levels has also been reported to be a prognostic indicator for multiple advanced solid tumors (De Vita *et al.*, Oncol Rep. 2000; 7(2):357-61). In addition to these cytokine investigations, studies by Elsasser-Beile *et al.*, 1993, *supra* have indicated that decreasing levels of serum IFN gamma protein correlate with increasing prostate tumor mass (Elsasser-Beile *et al.*, 1993), and the present inventors have detected mRNA levels of IFN-gamma in peripheral blood leukocytes that are consistent with this study (). The diseases described above, such as schizophrenia and cancer, can be considered complex disorders, in as much as multiple gene abnormalities contribute to the etiology. Genome scans are widely used in the search for linkage regions, as a prerequisite for identification and mutation screening of candidate susceptibility genes. Linkage studies possess a number of limitations, often including some lack of reproducible, strong linkage findings, and the large breadth of chromosomal areas identified, which can contain potentially hundreds of genes. It is also considered that multiple genes of small or moderate effect may contribute to for example schizophrenia susceptibility, and therefore each need to be identified. However, linkage studies have highlighted a number of chromosomal regions that may harbor genes that contribute to schizophrenia and cancer. The difficult task is to identify susceptibility alleles among the large numbers of genes within or near these regions. Sequence analysis and association testing for all the genes within regions of linkage would be an overwhelming task.

An alternatively investigation of candidate genes that does not rely on genetic linkage data, allows a potential direct route to discovery of a gene mutation that may be involved in the etiology and pathogenesis of a disease, for example schizophrenia (O'Donovan *et al.*, Am J Hum Genet 1999;65, 587-592). To date however, although plausible candidates, particularly neurotransmitter metabolism and transport pathway members, and genes implicated in neurodevelopment, have been investigated, no candidate gene to date has produced strong association with schizophrenia.

A few recent studies have explored the possibility of finding candidate genes for complex disorders and/or traits, by invoking a paradigm of candidate gene discovery or identification within regions of linkage, following or in parallel with measurement of gene expression of the tissue of interest. The paradigm of utilizing gene expression for the

identification of candidate disease genes was also explored by Blackshaw et al. in a study of gene expression in murine rod cells, to identify gene candidates for retinal diseases (Blackshaw et al., Cell 2001;107:579-89). The study, performed by serial analysis of gene expression (SAGE) found 264 previously uncharacterized genes that were expressed in the rod cells. Of those, 87 mapped to 37 different retinal disease loci, and are therefore considered candidate disease genes. In another study, Oestreicher et al. performed microarray gene expression using biopsied skin from patients with psoriasis and healthy controls and found 159 genes that were differentially expressed in the psoriasis biopsy samples. 27 of the differentially expressed genes mapped to psoriasis susceptibility loci, and were then considered as candidate genes for psoriasis (Oestreicher et al., Pharmacogenomics J. 2001; 1(4):272-87.). Additional problems with this approach however, are that for the analysis of, for example brain tissue for research in psychiatric disorders such as schizophrenia, research problems are encountered by investigators collecting post mortem brain samples, where the subject's physiological state at death can be poorly defined, and the delay between time of death and brain sample collection can be lengthy (Li et al., Hum Mol Genet. 2004 13(6):609-16). This can lead to variability between samples, as also recently reported by Loring et al., following a study of gene expression in brain tissue from Alzheimer's disease patients (Loring et al., DNA Cell Biol. 2001;20:683-95). In addition, biopsy would also be required for the analysis of tumor tissue for cancer research, and thus many subjects would have to undergo additional invasive surgery to obtain tissues for study.

### SUMMARY OF THE INVENTION

In one embodiment, the invention provides a method for evaluating a physical state of a subject (*e.g.*, a "test subject"). This method comprises comparing an expression profile of surrogate cells from the subject, with a normal expression profile of surrogate cells from a normal subject not having the physical state, wherein a difference between the expression profiles is indicative of the physical state of the test subject.

In an alternative embodiment, evaluating a physical state of a subject (*e.g.*, a "test subject"), which method involves comparing an expression profile of surrogate cells from the test subject with an expression profile of surrogate cells from a known subject or

subjects determined to have the physical state. In this case, similarity in the expression profiles indicates that the test subject has the physical state of the known subject or subjects

In yet another embodiment, the invention provides a method for evaluating a treatment or therapy, such as a therapeutic compound, in a test subject. This method  
5 comprises comparing an expression profile of surrogate cells from the subject after exposing the subject to the compound, with an expression profile of surrogate cells from the subject prior to exposure to the compound, wherein a difference in the expression profiles indicates an effect of the compound on the test subject. In a further aspect, this method compares the expression profile of the test subject after exposing the subject to the  
10 compound, with a normal expression profile of surrogate cells from a normal subject. Similarity of the expression profiles indicates a therapeutic benefit of the compound.

In yet another aspect, this method compares the expression profile of the test subject after exposing the subject to the treatment or therapy, with an expression profile of surrogate cells from other subjects with the same physical state following exposure to  
15 different therapies and improvement of physical state, wherein a similarity of the expression profiles is indicative of the treatment or therapy efficacy on the test subject. In another alternative method, the expression profile of the test subject after exposing the subject to the treatment or therapy, is compared with an expression profile of surrogate cells from other subjects with the same physical state following exposure to different therapies, and  
20 lack of improvement or worsening of the physical state. Similarity of the expression profiles indicates a lack of therapeutic benefit of the compound.

In yet another embodiment, the invention provides a method for predicting a response to treatment or therapy, which comprises comparing an expression profile from the test subject prior to exposing the subject to a treatment or therapy, with an expression  
25 profile from surrogate cells from other subjects with the same physical state also profiled prior to exposure to different therapies, wherein a similarity in the expression profiles predicts an effect of the treatment or therapy on the test subject based on the effect of that therapy on another subject or subjects having a similar pre-treatment expression profile. In a further aspect, this method would be employed for choice of treatments.

In yet another embodiment the present invention provides for a method of treating a disease, disorder or physical state or to prevent onset of a disease, disorder or physical state, comprising administering a nucleic acid found to have altered expression in surrogate tissues, between a test subjects with the physical state, and a normal subject or subjects, including, but not limited to gene therapy with nucleic acid transcripts, antisense mRNA, or other inhibitory RNAs.

In an additional embodiment, this invention provides a method for identifying nucleic acids containing sequence alterations that may have a role in the etiology of a disease or disorder or physical state, in the pathogenesis of, or in the susceptibility for developing a disease or disorder or physical state. This method comprises identifying a nucleic acid that has altered gene expression in surrogate cells from a test subject when compared to surrogate cells from a normal subject or subjects, and then comparing the genomic sequence of the nucleic acid, to identify the sequence change. In a further aspect, this nucleic acid may be found to map within the human genome within or close to or adjacent to a region that has been previously identified in a linkage study or genome scan, or associated with the disease, disorder or physical state. In yet another embodiments the present invention provides for a method of treating a disease, disorder or physical state, comprising administering a normal counterpart of a nucleic acid found to have a sequence change using methods described in this invention, including but not limited to gene therapy with nucleic acid transcripts, antisense mRNA, or other inhibitory RNAs.

According to the invention, the physical state can be a disease or disorder such as the presence of cancer, a neurological disorder, or a psychiatric or mood disorder, or other diseases, disorders or physical states. In specific embodiments exemplified *infra*, the physical state is prostate cancer, breast cancer, schizophrenia, bipolar disorder, or Alzheimer's disease. Naturally, the subject can be any multi-celled organism that can offer surrogate cells (as hereinafter defined); the examples demonstrate these methods in humans.

The surrogate cells can be, but are not limited to, peripheral blood leukocytes, such as monocytes, macrophages, lymphocytes, granulocytes, eosinophils neutrophils, and basophils, or other white blood cell types or subtypes. They can also be mucosal epithelia, skin, hair follicle, or CSF cells (which are predominantly leukocytes).

Various types of physical state evaluations can be made in accordance with the invention. For example, evaluating a physical state can involve diagnosing the presence of a disease or disorder, determining the prognosis of the subject, determining susceptibility of a subject for a disease or disorder, monitoring a therapy for a disease or disorder, developing or selecting a therapy for a disease or disorder, or classifying a disease or disorder.

Although the robust methods of the invention do not require it, the methods envision further testing for a biochemical marker of the physical state in the blood or some other tissue sample, or evaluating a biopsy tissue sample for the presence of the physical state.

The expression profiling can be accomplished using any technology to measure nucleic acid transcript levels. For example, the method could employ a nucleic acid microarray, such as an oligonucleotide microarray or a cDNA micorarray. Alternatively, one could simply employ reverse transcriptase-polymerase chain reaction (RT-PCR) or Northern blot hybridization. Additional methods that could be employed include, but are not limited to, Serial Analysis of Gene Expression (SAGE), high performance liquid chromatography (HPLC), mass spectrometry, differential display, quantative measures of allelic specific expression, Taqman assays, Molecular Beacon assays, and phage display.

### DESCRIPTION OF THE DRAWINGS

**Figure 1. TreeView Representation of Cluster patterns of gene expression among men with prostate cancer and age-matched control subjects. 1A.** Data are represented in matrix format. Each row represents a single gene (for space gene names have been omitted). Each column represents an experimental leukocyte patient or control sample. For each sample the ratio of the abundance of transcripts of each gene, to the median abundance of the genes's transcript among the individuals leukocytes, is represented by a rectangle in the corresponding matrix. The rectangles each represent the magnitude of the ratio relative to the median for the total set of samples. The dendrogram along the horizontal axis indicates the clusters of most similar subjects, based on gene expression levels of 1535 genes. The dendrogram along the vertical axis represents sample nodes of the total Cluster results, where genes appear together on the branches of the tree if they have similar patterns of gene expression. Example of Cluster nodes are taken from the

total TreeView data, showing genes that are generally expressed at lower levels in the prostate cancer samples (A1 to A13), than control subject samples (B1 to B7). 1B. A scaled representation of the horizontal dendrogram showing patient and control cluster results is shown.

5           **Figure 2A-B. TreeView representation of Cluster patterns of actual and randomized expression levels of 1535 genes.** Relationships among samples are represented by a dendrogram "tree", where branch lengths reflect the degree of similarity, such that short branch lengths between nodes indicate similarity between samples. The arrows indicate the direction of subject divergence along the branches from each node.

10           **Figure 3. Partial TreeView Representation of Cluster patterns of gene expression among SZ men and control subjects.** 3A Scaled representation of the horizontal dendrogram showing patient and control cluster results, based on the expression levels of 948 genes. Control Samples (C-401,492,536,634 and 641) cluster into one node, SZ samples (P- 493,494,495,535,588, 630, 631 and 964 (non-medicated subject)) cluster  
15 into a separate node. The sub-clusters within the SZ group do not seem to represent drug profiles, and the non-medicated subject (P-964) clusters within the SZ cluster node. The rectangles beneath each subject number represent the average signal intensity of a sample node of genes down regulated in SZ subjects.

20           **Figure 4. TreeView Representations of Cluster patterns of gene expression among SZ and BPD subjects.** Data are represented in matrix format. Each row represents a single gene (for space gene names have been omitted). Each column represents an experimental leukocyte sample. For each sample the ratio of the abundance of transcripts of each gene, to the median abundance of the genes's transcript among the individuals leukocytes, is represented a rectangle in the corresponding matrix. The  
25 rectangles each represent the magnitude of the ratio relative to the median for the total set of samples. The dendrogram along the horizontal axis indicates the clusters of most similar subjects, based on gene expression levels of 1002 genes. The dendrogram along the vertical axis represents nodes, where genes appear together on the branches of the tree if they have similar patterns of gene expression. 4A. Example of Cluster nodes taken from  
30 the total TreeView data, showing genes that are expressed at lower levels (green) or absent

(grey) in the SZ patients (SZ- 493, 494, 495, 535, 588, 630, 631, and 964 (non-medicated), than the leukocyte samples taken from men with BPD (BPD- 767, 846). **4B.** A scaled representation of the horizontal dendrogram showing subject cluster results.

**Figure 5. TreeView representation of Cluster patterns of actual and randomized expression levels of 1002 genes.** Relationships among samples are represented by a dendrogram "tree", where branch lengths reflect the degree of similarity, such that short branch lengths between nodes indicate similarity between samples. The arrows indicate the direction of subject divergence along the branches from each node. **5A.** A scaled representation of the horizontal dendrogram described in Figure 4, where BPD subjects (BPD-747, and 846) cluster in one sub-node. **5B.** A scaled representation of the TreeView readout generated when the gene expression levels of 1002 genes were randomized for each subject. Short branch length between nodes (in comparison to those observed in 5A) suggests only minor differences between samples.

**Figure 6.- The proportion of top ranked genes/ESTs that map to regions of schizophrenia linkage, filtered by increasing expression level cutoffs.** Genes/ESTs were sorted by t-test p value (lowest to highest). The dataset was then subjected to a filtering step using increasing stringency in the form of signal intensity cutoffs (20 intensity unit steps). For each intensity cutoff, genes/ESTs that did not have 2 or more subjects with expression levels  $\geq$  the cutoff value were removed, and the number of genes/ESTs that map to regions of schizophrenia linkage within the top 10 of all genes/ESTs that passed the filters, were then plotted on the Y axis for each intensity cutoff level (X-axis). Filled grey circles indicate the sum total of linked genes/ESTs for each intensity cutoff. Thirty sets of randomized linkage data were also analyzed at each intensity cutoff point, and are shown by the filled black circles.

### **DETAILED DESCRIPTION**

The present invention provides novel "gene signatures" that are indicative of a physical state, *e.g.*, a disease or disorder of a subject. These gene signatures, or



expression profiles, are obtained from surrogate cells, such as blood cells, mucosal epithelial cells, and the like, that are available through non-invasive or minimally invasive procedures. Using the power of informative multiple gene expression profiling, or alternatively the coupling of multiple single gene expression measurements, the expression profile as described in the present invention permits the accurate classification, diagnosis, staging, and prognosis of diseases, determination of a biological, psychiatric, neurological or physical state including aging. The present invention also permits the prediction and evaluation of efficacy of therapeutic and treatment regimens and monitoring of subjects, and evaluation of candidate compounds for development and/or use as therapeutics. This invention also allows for the identification of candidate nucleic acids involved in the etiology and or susceptibility for a physical state.

This invention has significant advantages over current diagnostic and prognostic technologies. It does not require highly invasive techniques, such as tumor biopsy, that are required for confirming diagnosis of a cancer or other tissue conditions. Furthermore, it provides a biological measurement that permits a more conclusive diagnosis of diseases and conditions that are presently only conditionally diagnosed with confirmation available only upon post-mortem examination, such as Alzheimer's disease, or for which no specific biological markers may be available, such as schizophrenia. In addition, this approach for discovery and validation of candidate genes for a physical state, utilizes a surrogate tissue, and therefore expands diagnostic choice and does not depend on the ability to access postmortem brain tissue, biopsied tumor tissue, or other involved tissues through invasive procedures. Indeed, invasive mechanisms of collection can greatly effect downstream gene expression, leading to great variability and inconsistencies between samples. The present invention is based, in part, on experiments which gave a complete classification of peripheral leukocyte expression clusters of prostate cancer patients (irrespective of race) when compared to age- and race-matched normal controls, and a classification into expression clusters for schizophrenia and bipolar disorder patients compared to age- and race-matched controls (in this case with no significant effect of drug treatment for the schizophrenia on the expression profiles). Furthermore, the expression clusters of the schizophrenia subjects were distinct from those of the bipolar subjects.

In particular, for both prostate cancer and the psychiatric conditions, specific patterns, or signatures, of leukocyte gene expression that can both distinguish between control subjects and patients, and also differentiate between different psychiatric illnesses, have been identified.

5 Experiments showing the accurate classification of prostate cancer patients and healthy control subjects into their respective groups, based on the expression levels of over 1500 genes, support breast cancer diagnosis through leukocyte expression signatures. Specifically, while the genes employed above for classification of prostate cancer will not necessarily be the exact genes employed for classification of breast cancer, common  
10 similarities between breast and prostate cancer, including incidence and mortality rates, risk factors, initiation of transformation, and roles of androgens and estrogens (reviewed in Lopez-Otin & Diamandis 1998; Coffey S. 2001; Cavalieri & Rogan. 2002; Liao *et al.*, 2002; Grover & Martin 2002) indicate that growth and development of a breast cancer will exert an effect on the immune system, similar to that predicted for prostate cancer, that can  
15 be detected at the level of altered gene expression in peripheral blood leukocytes.

It seems clear that the use of multiple nucleic acid transcripts for the determination of expression signatures provides considerably more detailed information on disease stage and prognosis than can be provided by the quantitation of individual serum protein levels, as described in the Background to the Invention. It should also be noted that although  
20 surrogate cell gene expression levels will be measured, if, *e.g.*, malignant breast cells were also present in the blood of patients, then gene expression of these cells will also be quantified. It seems likely that the detection of gene expression in affected cells within blood might actually increase the specificity of the analysis, as mRNA levels arising from circulating involved cells would differ from mRNA levels in prostate cancer patients with  
25 no such cells in their blood stream, and to a even greater degree than normal control subjects.

These results form the basis of a diagnostic screen. A clinical assay would initially involve extraction of a surrogate tissue, such as a blood sample, from the subject at risk for the condition to be tested. A labeled probe synthesized from RNA extracted from the  
30 surrogate cells can be hybridized to a microarray containing a number of genes (determined

according to this invention) that are differentially expressed between patients and control individuals to identify whether the test subject has the particular condition. The resultant expression pattern can then be compared to a set of known multigene signatures that more specifically characterize the condition, *e.g.*, expression profiles that are specific for individual stages of tumor progression. The invention represents a non-invasive diagnostic assay that can yield both diagnostic and staging information for each individual at risk.

Since this assay will measure gene expression within surrogate cells such as leukocytes, instead of cells directly involved in the physical state, and does not rely on the measurement of biomolecules secreted from involved cells, the resultant assay is sensitive and accurate, and capable of detecting conditions that are still at an early stage. Such an assay serves as an important pre-screen that can, with a minimum of patient discomfort, identify subjects who have the particular condition.

## DEFINITIONS

### *Specialized*

As used herein, the term "physical state" refers to the physiological, psychological, and health status of a subject. Various physical states include diseases and disorders, such as: proliferative disorders including cancer; pulmonary disorders; dermatological diseases; developmental disorders; muscular disorders; respiratory diseases; sexual, fertility and gynecological disorders; allergic disorders; inflammatory disorders (*e.g.* ulcerative colitis etc.); infectious diseases; parasitic infestations; growth abnormalities, a hyperactive or hypoactive endocrine syndrome (*e.g.*, hyperthyroidism, hypothyroidism, growth hormone deficiency or dwarfism, type I diabetes, type II diabetes, etc.); neurological diseases (*e.g.*, Alzheimer's, Parkinson's, Huntington's, ALS, etc.); psychiatric and mood disorders (*e.g.*, schizophrenia, bipolar disorder, depression, obsessive-compulsive disorder, etc.); obesity; sleep disorders; other pathological conditions; and normal and abnormal aging. Physical states also include altered metabolic states, which may be due to ingestion of exposure to, pharmaceuticals, chemicals, alcohol, environmental toxins, food toxins, and the like; metabolic or nutritional conditions or deficiencies, such as but not limited to hyperlipidemia, hypercholesterolemia, malnutrition, and vitamin deficiencies. The data show a possible heirarchy of effects: a disease like schizophrenia seems to have greater

impact on expression profiles of blood cells than the neuroleptic drugs that the schizophrenic patients are taking for the condition. A normal physiological state is a special kind of physical state, which can be determined from the methods of the invention.

The term "expression profile" refers to expression of two or more, preferably three or more, for example 5, 10, 20, 50, 100, 500, or 1000 or more, genes/EST or other transcribed nucleic acids. Genes/ESTs or nucleic acids within a subject's expression profile can be expressed at different levels (either to a greater or lesser extent, *e.g.*, by about 2-fold of more, or less than 2-fold, and preferably within the error limits of the detection) to the gene expression profile levels of a subject or subjects with a physical state, and also for example, between subjects treated with therapeutic compounds, or between treated and untreated subjects. The differences between subjects expression profiles can then for example, be employed for diagnosing the presence of a physical state, determining the prognosis of the subject, determining susceptibility of a subject for a physical state, monitoring a therapy for a physical state, developing or selecting a therapy for a physical state, or classifying a physical state. In certain embodiments, genes in an expression profile may not include known markers of the involved cells, *e.g.*, PSA in prostate cancer (given the highly sensitive detection technologies available, efforts are made to detect cancer cell genes in the low population of circulating metastatic cells), but in early stage non-disseminated disease such markers may well be expressed in the surrogate cells and be informative. The expression profile is indicative of a particular physical state. As used herein, the expression profile of a gene is preferably the level of mRNA, *e.g.*, measured using microarrays or RT-PCR as described herein. . In particular embodiments, nucleic acids (*e.g.*, mRNA) expressed by a cell are reverse transcribed into either cDNA or cRNA, and the abundances of the cDNA and/or cRNA molecules are measured. Expression profiles can be presented in various forms, as discussed below, including through dendograms, TreeView readouts, color matrixes, charts, graphs, or by computer analysis without visualization. Determination of expression profiles involves analyzing expression of genes in subjects diagnosed, for example using statistical analyses, or heirarchical clustering or classification algorithms (with as much accuracy and precision as possible, including through post-mortem confirmation if necessary) with the particular physical state.

As used herein, the term "surrogate cells" refers to cells from a tissue source that is not the primary involved tissue of the physical state of the subject (except of course to the extent that "normal" is a special type of physical state, then the surrogate cells exhibit "normal" expression patterns). The term includes but need not be limited to blood cells, mucosal epithelial cells, skin cells, cells of hair follicles, cells from cerebrospinal fluid (CSF), and cells from lymphatic fluid. One of the advantages of the invention lies in the power to analyze expression patterns from complex mixtures of cells that might be present in any given tissue source, as discussed in the Examples. Thus, blood cells include leukocytes (monocytes, macrophages, lymphocytes, granulocytes, eosinophils, etc.), as well as platelets and megakaryocytes. Skin cells include Langerhans cells, keratinocytes, and dermal cells. Furthermore, the surrogate cells can be purified populations or subpopulations of these cells, *e.g.*, T or B lymphocytes separated from the blood cells. However, this is not necessary for practicing the invention.

Surrogate cells are predominantly not the cells affected by the physical state (except, of course, for a normal physical state or normal aging) but the term does not exclude the possibility that disease cells are present in the surrogate cells. Thus, if the disease is cancer and the surrogate cells are blood cells, there may be some metastatic cells in the blood cells. However, tumor cells from a biopsy would clearly not be surrogate cells for purposes of this invention. Furthermore, purification of involved cells is not necessary, and falls outside the definition of surrogate cells.

The term "subject" can mean patient, test subject, animal including laboratory animals, or any entity capable of testing for physical state by obtaining an expression profile or signature of surrogate cells, including plants, for example, a genetically modified plant species. Preferably a patient is a human, but can also be a domestic animal or pet (*e.g.*, a dog, cat, etc.), a farm animal (*e.g.*, horse, cow, sheep, pig, goat, etc.), or a wild animal, such as in a zoo. A test subject can be a human or animal involved in a clinical trial of a drug or in a trial, as exemplified herein, for determining new, expanded, or refined expression profiles. Clearly the groups of "patients" and "test subjects" can overlap. Laboratory animals include mice, rats, rabbits, hamsters, cats, dogs, etc.

The term "genetically linked" refers to the proximity of two or more genes and/or traits within the genome of an organism that causes those genes or traits to be inherited, transferred, or moved together with a frequency greater than for genes or traits not linked.

The linkage is a continuous variable and is inversely related to the distance between

5 genes/traits on the genome. For investigating linkage of diseases, disorders or physical states, such as schizophrenia, genetic linkage is measured by the heritability within a family (and families) of genes or markers of interest, whereby genes or markers within a particular chromosome location are linked to a disease, disorder or physical state if allelic variation of the gene or marker segregates within the family with the disease, disorder or physical state.

10 Those genomic regions are considered likely to contain genes which, when mutated or altered or deleted, contribute to susceptibility, or the cause or pathogenesis or etiology of a disease, disorder or physical state. For example, for schizophrenia linkage has been suggested for multiple genomic regions including chromosomes 1q23.3-q31.1, 2p12-q22.1, 3p25.3-p22.1, 5q23.2-q34, 11q22.3-24.1, 6pter-p22.3, 2q22.1-q23.3, 1p13.3-

15 q23.3, 8p22-p21.1, 6q15-q23.2, 6p22.3-p21.1, 10pter-p14, 14pter-q13.1, 15q21.3-q26.1, 16p13-q12.2, 17q21.33-q24.3, 18q22.1-qter, 20p12.3-p11, 22pter-q12.3 (Lewis et al., Am J Hum Genet. 2003;73(1):34-48) According to one embodiment of the presently claimed methods, nucleic acids representing genes or ESTs that have a different expression profiles in surrogate cells from a subject having or suspected of having a physical state compared

20 with cells from normal individuals not having a physical state, which can also be linked to that disease, disorder or physical state, will be chosen for genetic mutation analysis, i.e., by sequencing. As used herein, the term genetically linked also includes nucleic acid sequences representing genes or ESTs on chromosomal regions that are proximal or distal to the linked site.

25 In a specific embodiment, exemplified below, one can identify relevant genes whose expression is up- or down-regulated in disease conditions such as prostate cancer or disorders such as schizophrenia. For further diagnosis and testing, one can prepare arrays with all or a subset of all of the genes. For example, such an array employs a probe for at least one such gene, preferably at least 5, more preferably at least 10, more preferably at

30 least 50, and more preferably at least 100, or 500, or 1000 or more such genes.

Furthermore, genes are selected for inclusion in an array on the basis of the significance

level of the differential expression. A significance level of less  $p < 0.1$  (e.g., using the Student's two-tailed test) indicates a trend towards significance; a significance level of  $p < 0.05$  provides greater certainty; a significance level of  $p < 0.01$  even greater certainty. It should be understood that the value of  $p$  may change with greater sample size.

5           Thus, in one embodiment, one can diagnose the presence of prostate cancer using expression data for one or more, preferably 5 or more, more preferably 10, 50, or 100 or more genes from Table 1, below. Preferably, the genes are selected as having a trend level of  $p < 0.1$ , or more preferably a significance level of  $p < 0.05$ , and more preferably  $p < 0.01$ . In one embodiment, the gene probe on the expression array detects one or more of

10   proteasome (prosome, macropain) subunit, alpha type, 5; S-phase kinase-associated protein 1A (p19A); KIAA0542 gene product; endothelial differentiation, G-protein-coupled receptor 6; tubulin, alpha 1 (testis specific); chromosome 10 open reading frame 6; G-rich RNA sequence binding factor 1; Rab acceptor 1 (prenylated); solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7; cAMP responsive

15   element modulator; Wiskott-Aldrich syndrome (eczema-thrombocytopenia); glutamate receptor, metabotropic 4; dynamin 2; glycosyltransferase AD-017; dimethylarginine dimethylaminohydrolase 2; similar to transcription factor TBX10; Tubulin, Alpha 1, Isoform 44; pyruvate kinase, muscle; splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor); ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature

20   sensitivity complementing); huntingtin-associated protein 1 (neuroan 1); ubiquitin ligase E3 alpha-II; ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast); potassium voltage-gated channel, shaker-related subfamily, beta member 2; farnesyltransferase, CAAX box, alpha; ATPase, H<sup>+</sup> transporting, lysosomal 16kDa, V0 subunit c; eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa; and likely ortholog of mouse variant

25   polyadenylation protein CSTF-64. In another embodiment, an expression array of the invention can include any genes with a significance of e.g.  $p < 0.0005$ , or alternatively with a significance of  $p < 0.001$ , or a trend level of significance of  $p < 0.07$ , from Table 1.

30           Thus, in one embodiment, one can diagnose the presence of schizophrenia using expression data for one or more, preferably 5 or more, more preferably 10, 50, or 100 or more genes from Table 2, below. Preferably, the genes are selected as having a trend level

of  $p < 0.1$ , or more preferably a significance of  $p < 0.05$ , and more preferably  $p < 0.01$ . In one embodiment, the gene probe on the expression array detects one or more of par-6 partitioning defective 6 homolog alpha (*C.elegans*) (also called homo sapiens tax interaction protein 40), transmembrane 4 superfamily member tetraspan NET-5, neural cell  
5 adhesion molecule 1, cadherin 16, KSP-cadherin WD repeat domain 1, growth hormone releasing hormone B-cell translocation gene 1, anti-proliferative solute carrier family 10 (sodium/bile acid cotransporter family), and member 1 HRIHFB2206 protein. In another embodiment, an expression array of the invention can include any genes with a significance of e.g.  $p < 0.0005$ , or alternatively with a significance of  $p < 0.001$ , or a trend level of  
10 significance of  $p < 0.07$ , from Table 2.

### *Generalized*

The terms used in this specification generally have their ordinary meanings in the art, within the context of this invention and in the specific context where each term is used. Certain terms are discussed below, or elsewhere in the specification, to provide additional  
15 guidance to the practitioner in describing the compositions and methods of the invention and how to make and use them.

As used herein, the term "isolated" means that the referenced material is removed from the environment in which it is normally found. Thus, an isolated biological material can be free of cellular components, *i.e.*, components of the cells in which the material is  
20 found or produced. In the case of nucleic acid molecules, an isolated nucleic acid includes isolated DNA, a PCR product, isolated RNA (mRNA, cRNA, tRNA, rRNA), a cDNA, or a restriction fragment. In another embodiment, an isolated nucleic acid is preferably excised from the chromosome in which it may be found, and more preferably is no longer joined to non-regulatory, non-coding regions, or to other genes, located upstream or  
25 downstream of the gene contained by the isolated nucleic acid molecule when found in the chromosome. In yet another embodiment, the isolated nucleic acid lacks one or more introns. Isolated nucleic acid molecules include sequences inserted into plasmids, cosmids, artificial chromosomes, and the like. Thus, in a specific embodiment, a recombinant nucleic acid is an isolated nucleic acid. An isolated protein may be associated with other  
30 proteins or nucleic acids, or both, with which it associates in the cell, or with cellular



membranes if it is a membrane-associated protein. An isolated organelle, cell, or tissue is removed from the anatomical site in which it is found in an organism. An isolated material may be, but need not be, purified.

5 The term "purified" as used herein refers to material that has been isolated under conditions that reduce or eliminate the presence of unrelated materials, *i.e.*, contaminants, including native materials from which the material is obtained. For example, a purified nucleic acid molecule is preferably substantially free of proteins or other unrelated nucleic acid molecules with which it can be found within a cell. As used herein, the term "substantially free" is used operationally, in the context of analytical testing of the material.  
10 Preferably, purified material substantially free of contaminants is at least 50% pure; more preferably, at least 90% pure, and more preferably still at least 99% pure. Purity can be evaluated by chromatography, gel electrophoresis, immunoassay, composition analysis, biological assay, mass spectrometry and other methods known in the art.

15 Methods for purification are well known in the art. For example, nucleic acids can be purified by precipitation, chromatography (including preparative solid phase chromatography, oligonucleotide hybridization, and triple helix chromatography), ultracentrifugation, and other means. A purified material may contain less than about 50%, preferably less than about 75%, and most preferably less than about 90%, of the cellular components with which it was originally associated. The "substantially pure" indicates the  
20 highest degree of purity which can be achieved using conventional purification techniques known in the art.

A "sample" as used herein refers to a biological material which can be tested, *e.g.*, a tissue, for example a surrogate tissue, comprising cells, that are tested or analyzed for the presence or absence of certain particular nucleic acid sequences, corresponding to certain  
25 genes that may be expressed by the cell or present in the cell.

A "gene" is a sequence of nucleotides which code for a functional "gene product". Generally, a gene product is a functional protein. However, a gene product can also be another type of molecule in a cell, such as an RNA. For the purposes of the present invention, a gene product also refers to an mRNA sequence which may be found in a cell.

For example, measuring gene expression levels according to the invention may correspond to measuring mRNA levels.

The term “express” and “expression” means allowing or causing the information in a gene or DNA sequence to become manifest, for example producing RNA (such as mRNA) or a protein by activating the cellular functions involved in transcription and translation of a corresponding gene or DNA sequence. A DNA sequence is expressed by a cell to form an “expression product” such as an RNA (*e.g.*, an mRNA) or a protein. The expression product itself, *e.g.*, the resulting RNA or protein, may also said to be “expressed” by the cell. As used herein, the term expression also refers to the amount or abundance of mRNA corresponding to a particular gene that is present in a cell.

“Amplification” of a nucleic acid, as used herein, denotes the use of an amplification synthetic process, such as polymerase chain reaction (PCR), to increase the concentration of a particular DNA or cDNA, or mRNA or cRNA sequence within a mixture of nucleic acid sequences. For a description of PCR see Saiki *et al.*, Science 1988, 239:487.

The term “inhibitory RNA” can refer to an RNA species that can directly or indirectly inhibit expression of a gene or other nucleic acids by interfering with, or decreasing the process of transcription, and/or directly or indirectly increasing the degradation or cleavage of the targeted gene or nucleotide transcript, thus reducing the gene or nucleic acid’s transcript levels or expression levels at the RNA and/or protein level. RNA molecules can be used to cause inhibition of expression of genes or other nucleotide sequences. RNA molecules utilized or employed for inhibition, can contain in whole or part, sequence that is at least similar to, or substantially identical to, or substantially complementary to (in whole or part), an RNA sequence produced from a gene or other nucleotide sequence being targeted (Shuey et al. Drug Discov Today. 2002 7(20):1040-6). Sequence-specific, or partially sequence specific inhibition of a gene or nucleotide transcript’s expression, can be induced using several different methodologies and molecule types, including but not limited to: chemically modified antisense oligodeoxyribonucleic acids (ODNs), ribozymes and siRNAs, peptide nucleic acids (PNAs), morpholino phosphorodiamidates, DNAzymes and 5'-end-mutated U1 small nuclear RNAs (Dorsett et

al. *Nat Rev Drug Discov.* 2004 3(4):318-29). Additionally, the introduction of single or double stranded RNA or RNA-like molecules that are preferably less than 30 nucleotides in length may be more useful for decreasing cell death and/or activation when the sequences are introduced. (Xu et al., *Biochem Biophys Res Commun.* 2004 316(3):680-7). The use of interference technologies such as RNAi for therapeutic approaches to physical states, diseases or disorders, can also include the introduction to cells, organs, tissues or organisms, of specific RNA molecules, either as uncomplexed oligonucleotides, and/or using viral or retroviral vectors, or other vectors such as plasmids or liposomes, containing small interfering RNA sequence (siRNA) or small hairpin RNA sequence (shRNA) or their precursor vector sequences (reviewed in Devroe et al., *Expert Opin Biol Ther.* 2004 4(3):319-27; Davidson et al., *Lancet Neurol.* 2004 (3):145-9).

A nucleic acid molecule is "hybridizable" to another nucleic acid molecule, such as a cDNA, oligo-DNA, or RNA, when a single stranded form of the nucleic acid molecule can anneal to the other nucleic acid molecule under the appropriate conditions of temperature and solution ionic strength (see Sambrook *et al.*, *supra*). The conditions of temperature and ionic strength determine the "stringency" of the hybridization. For preliminary screening for homologous nucleic acids, low stringency hybridization conditions, corresponding to a  $T_m$  (melting temperature) of 55 °C, can be used, *e.g.*, 5x SSC, 0.1% SDS, 0.25% milk, and no formamide; or 30% formamide, 5x SSC, 0.5% SDS). Moderate stringency hybridization conditions correspond to a higher  $T_m$ , *e.g.*, 40% formamide, with 5x or 6x SCC. High stringency hybridization conditions correspond to the highest  $T_m$ , *e.g.*, 50% formamide, 5x or 6x SCC. SCC is a 0.15M NaCl, 0.015M Na citrate. Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of  $T_m$  for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher  $T_m$ ) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating  $T_m$  have been derived (see Sambrook *et*

*al.*, *supra*, 9.50-9.51). For hybridization with shorter nucleic acids, *i.e.*, oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (see Sambrook *et al.*, *supra*, 11.7-11.8). A minimum length for a hybridizable nucleic acid is at least about 10 nucleotides; preferably at least about 15  
5 nucleotides; and more preferably the length is at least about 20 nucleotides.

Suitable hybridization conditions for oligonucleotides (*e.g.*, for oligonucleotide probes or primers) are typically somewhat different than for full-length nucleic acids (*e.g.*, full-length cDNA), because of the oligonucleotides' lower melting temperature. Because the melting temperature of oligonucleotides will depend on the length of the oligonucleotide  
10 sequences involved, suitable hybridization temperatures will vary depending upon the oligonucleotide molecules used. Exemplary temperatures may be 37° C (for 14-base oligonucleotides), 48° C (for 17-base oligonucleotides), 55° C (for 20-base oligonucleotides) and 60° C (for 23-base oligonucleotides). Exemplary suitable hybridization conditions for oligonucleotides include washing in 6x SSC/0.05% sodium  
15 pyrophosphate, or other conditions that afford equivalent levels of hybridization.

Preferably, nucleic acid molecules in the present invention are detected by hybridization to probes of a microarray. Hybridization and wash conditions are therefore preferably chosen so that the probe "specifically binds" or "specifically hybridizes" to a specific target nucleic acid. In other words, the nucleic acid probe preferably hybridizes,  
20 duplexes or binds to a target nucleic acid molecules having a complementary nucleotide sequence, but does not hybridize to a nucleic acid molecules having a non-complementary sequence. As used herein, one oligonucleotide sequence is considered complementary to another when, if the shorter of the oligonucleotides is less than or equal to about 25 bases, there are no mismatches using standard base-pairing rules, or using mismatch analysis  
25 algorithms (Affymetrix Inc). If the shorter of the two polynucleotides is longer than about 25 bases, there is preferably no more than a 5% mismatch. Preferably, the two oligonucleotides are perfectly complementary (*i.e.*, no mismatches). It can be easily demonstrated that particular hybridization conditions are suitable for specific hybridization by carrying out the assay using negative controls. See, for example, Shalon *et al.*, Genome  
30 Research 1996, 639-645; and Chee *et al.*, Science 1996, 274:610-614.

Optimal hybridization conditions for use with microarrays will depend on the length (*e.g.*, oligonucleotide versus polynucleotide greater than about 200 bases) and type (*e.g.*, RNA, DNA, PNA, etc.) of probe and target nucleic acid. General parameters for specific (*i.e.*, stringent) hybridization conditions are described above. Hybridization conditions for use of Affymetrix commercial oligonucleotide arrays have been developed for standardized use (Affymetrix Inc.) For cDNA microarrays, such as those described by Schena *et al.* (Proc. Natl. Acad. Sci. USA; 1996, 93:10614), typical hybridization conditions comprise hybridizing in 5x SSC and 0.2% SDS at 65 °C for about four hours, followed by washes at 25°C in a low stringency wash buffer (for example, 1x SSC and 0.2% SDS), and about 10 minutes washing at 25°C in a high stringency wash buffer (for example, 0.1x SSC and 0.2% SDS). Useful hybridization conditions are also provided, *e.g.*, in Tijessen, Hybridization with Nucleic Acid Probes, Elsevier Sciences Publishers (1996), and Kricka, Nonisotopic DNA Probe Techniques, Academic Press, San Diego CA (1992). Generally commercially available expression screening systems that use hybridization provide defined hybridization and wash conditions.

### MEASURING EXPRESSION PROFILES

Various commercial systems are available for profiling gene expression. These include the powerful single gene amplification processes such as reverse transcription-polymerase chain reaction (RT-PCR). Multigene profiling can be performed in single reaction mixtures using specific detection signals, such as dyes, in separate reaction mixtures, or on arrays. Various commercial systems are available for expression profiling as well.

eXrpress Profiling (XP) by Althea (San Diego, CA) is useful in screening large numbers of compounds for effects on expression of a limited number of known target genes (approximately up to 20 per single well reaction). The assay employs discernible fluorescent dyes that can be reliably and simultaneously detected in a single reaction mixture. XP works by first amplifying the cDNA sources to be compared with a pair of gene-specific primers that each carry a universal sequence at their 5' end. The resulting PCR amplicon is then further amplified with a pair of primers that hybridize to the

universal sequences at both termini of the original PCR amplicon. One of the latter primer pair is fluorescently labeled, such that the final product can be quantified.

Assays-on-Demand™ by Applied Biosystems (Foster City, CA) can be used for validation of microarray hits. The assay provides a means of higher reliability and accuracy in the expression profiling of single genes. Each kit is custom tailored to a particular gene; kits can be combined for multigene profiles. It is useful for standardization purposes, due to better comparability of results between different experiments/laboratories. The assay uses random primers in the initial cDNA synthesis step, which enables higher quality signal detection along the transcript. The PCR amplification step is based on AB's TaqMan system which then allows one to quantify the amount of cDNA in the sample.

EnzyStart™ by GeneCopeia (Frederick, MD) blocks the 3' end of amplification primers with an enzymatically removable blocking group, which avoids non-specifically primed DNA polymerization that may otherwise occur due to primer hybridization at ambient temperature. A Terminal Blocker Group Remove Enzyme (TBGRE) present in the reaction is activated at temperatures above 55°C to produce free hydroxyl-groups at the 3' end of the primer, thus allowing the PCR reaction to start only after non-specifically hybridized primers are melted off the template. This is particularly useful when very low concentrations of cDNA are to be detected, when signal to noise ratio is a problem.

Omega Beacon™ by Gorilla Genomics (Alameda, CA) provides a quantitative real-time PCR method useful for measurement of gene expression. These probes form stem-loop structures, where the loop sequence hybridizes specifically to the DNA target of interest. Upon hybridization the stem is destabilized and opens, which releases a fluorescence quencher from the proximity of the fluorophore, and thus allowing for fluorescence and the quantification thereof.

Black Hole Quenchers by Biosearch Technologies (Novato, CA) employs on a similar mechanism as Omega Beacons. Here fluorophore and quencher are kept in proximity in the unhybridized state due to the random coiling of the probe. Upon hybridization to the target sequence the probe is stretched out, which permits quantifiable fluorescence emission.

### *Nucleic Acid Arrays*

The terms “array” and “microarray” are used interchangeably and refer generally to any ordered arrangement (*e.g.*, on a surface or substrate) or different molecules, referred to herein as “probes”. Each different probe of an array specifically recognizes and/or binds to a particular molecule, which is referred to herein as its “target”. Microarrays are therefore useful for simultaneously detecting the presence or absence of a plurality of different target molecules, *e.g.*, in a sample. In preferred embodiments, arrays used in the present invention are “addressable arrays” where each different probe is associated with a particular “address”. For example, in preferred embodiments where the probes of are immobilized on a surface or a substrate, each different probe of the addressable array may be immobilized at a particular, known location on the surface or substrate. The presence or absence of that probe’s target molecule in a sample may therefore be readily determined by simply determining whether a target has bound to that particular location on the surface or substrate.

The methods of the invention may be practiced using nucleic acid arrays (also referred to herein as “transcript arrays” or “hybridization arrays”) that comprise a plurality of nucleic acid probes immobilized on a surface or substrate. The different nucleic acid probes are complementary to, and therefore hybridize to, different target nucleic acid molecules, *e.g.*, in a sample. Thus such probes may be used to simultaneously detect the presence and/or abundance of a plurality of different nucleic acid molecules in a sample, including the expression of a plurality of different genes; *e.g.*, the presence and/or abundance of different mRNA molecules, or of nucleic acid molecules derived therefrom (for example, cDNA or cRNA).

There are two major types of microarray technology; spotted cDNA arrays and manufactured oligonucleotide arrays. Examples 1 and 2 employ high density oligonucleotide Affymetrix® GeneChip arrays (reviewed in Schena *et al.*, 1998).

***Transcript Arrays Generally.*** In a preferred embodiment the present invention makes use of “transcript arrays” (also called herein “microarrays”) for determining the effect of a test compound on gene expression. Transcript arrays can be employed for analyzing the transcriptional state in a surrogate cell in comparison to a known cell

(whether known to be normal or known to be from a subject with an abnormal physical state).

Microarrays can be made in a number of ways, of which several are described below. However produced, microarrays share certain characteristics. The arrays are preferably reproducible, allowing multiple copies of a given array to be produced and easily compared with each other. Preferably the microarrays are small, usually smaller than 5 cm<sup>2</sup>, and they are made from materials that are stable under binding (*e.g.*, nucleic acid hybridization) conditions. A given binding site or unique set of binding sites in the microarray will specifically bind the product of a single gene in the cell. Although there may be more than one physical binding site (hereinafter "site") per specific mRNA, for the sake of clarity the discussion below will assume that there is a single site. It will be appreciated that when cDNA complementary to the RNA of a cell is made and hybridized to a microarray under suitable hybridization conditions, the level of hybridization to the site in the array corresponding to any particular gene will reflect the prevalence in the cell of mRNA transcribed from that gene. For example, when detectably labeled (with a fluorophore) cDNA complementary to the total cellular mRNA is hybridized to a microarray, the site on the array corresponding to a gene (*i.e.*, capable of specifically binding a nucleic acid product of the gene) that is not transcribed in the cell will have little or no signal, and a gene for which the encoded mRNA is prevalent will have a relatively strong signal.

The use of a two-color fluorescence labeling and detection scheme to define alterations in gene expression has been described (*e.g.*, Shena *et al.*, Science 1995, 270:467-470). An advantage of using cDNA labeled with two different fluorophores is that a direct and internally controlled comparison of the mRNA levels corresponding to each arrayed gene in two cell states can be made, and variations due to minor differences in experimental conditions (*e.g.*, hybridization conditions) will not affect subsequent analyses. However, it will be recognized that it is also possible to use cDNA from a single cell, and compare, for example, the absolute amount of a particular mRNA in, *e.g.*, a treated and untreated cell..



By way of example, GeneChip expression analysis (Affymetrix, Santa Clara, CA) generates data for the assessment of gene expression profiles and other biological assays. Oligonucleotide expression arrays simultaneously and quantitatively interrogate thousands of mRNA transcripts (genes or ESTs, via a cRNA synthesis step), simplifying large  
5 genomic studies. Each transcript can be represented on a probe array by multiple probe pairs, representing different regions of the genes or ESTs, to differentiate among closely related members of gene families. Each probe cell contains millions of copies of a specific oligonucleotide probe, permitting the accurate and sensitive detection of low-intensity mRNA hybridization patterns. After hybridization intensity data is captured, *e.g.*, using a  
10 Hewlett-Packard GeneArray™ scanner, software can be used to automatically calculate intensity values for each probe cell. Probe cell intensities can be used to calculate an average intensity for each gene, which directly correlates with mRNA abundance levels. Expression data can be quickly sorted on any analysis parameter and displayed in a variety of graphical formats for any selected subset of genes. Other gene expression detection  
15 technologies include the research products manufactured and sold by Perkin-Elmer and Gene Logic. Additionally, software such as BRB Array Tools (NCI), GeneSpring (Silicon Genetics), GeneLinker Platinum (Predictive Patterns Software Inc.) can also be used to perform clustering, gene profiling, sample classification and statistical analyses of expression profiles.

20 ***Preparation of Microarrays.*** Microarrays are known in the art and preferably comprise a surface to which short or long oligonucleotide or cDNA probes, that correspond in sequence to gene products (*e.g.*, cDNAs, mRNAs, cRNAs, polypeptides, and fragments thereof), can be specifically hybridized or bound at a known position within the microarray. In one embodiment, the microarray is an array in which each position represents a discrete  
25 binding site for a product encoded by a gene (*e.g.*, a protein or RNA), and in which binding sites are present for products of most or almost all of the genes in the organism's genome. In a preferred embodiment, the "binding site" (hereinafter, "site") is a nucleic acid or nucleic acid analogue to which a particular cognate cDNA or cRNA can specifically hybridize. The nucleic acid or analogue of the binding site can be, *e.g.*, a synthetic  
30 oligomer, a full-length cDNA, a less-than full length cDNA, or a gene fragment.

Although in a preferred embodiment the microarray contains binding sites for products of all or almost all genes in the target organism's genome, such comprehensiveness is not necessarily required for diagnostic arrays with a defined set of genes that are differentially expressed (the expression profile genes).

5           **Preparing Nucleic Acids for Microarrays.** As noted above, the "binding site" to which a particular cognate cDNA or cRNA specifically hybridizes is usually a nucleic acid or nucleic acid analogue attached at that binding site. In one embodiment, the binding sites of the microarray are DNA polynucleotides corresponding to at least a portion of each gene in an organism's genome. These DNAs can be obtained by, *e.g.*, polymerase chain  
10 reaction (PCR) amplification of gene segments from genomic DNA, cDNA (*e.g.*, by RT-PCR), or cloned sequences. PCR primers are chosen, based on the known sequence of the genes or cDNA, that result in amplification of unique fragments (*i.e.*, fragments that do not share more than 10 bases of contiguous identical sequence with any other fragment on the microarray). Computer programs are useful in the design of primers with the required  
15 specificity and optimal amplification properties. See, *e.g.*, Oligo version 5.0 (National Biosciences). In the case of binding sites corresponding to very long genes, it will sometimes be desirable to amplify segments near the 3' end of the gene so that when oligo-dT primed cDNA probes are hybridized to the microarray, less-than-full length probes will bind efficiently. Typically each gene fragment on the microarray will be between about 50  
20 bp and about 2000 bp, more typically between about 100 bp and about 1000 bp, and usually between about 300 bp and about 800 bp in length. PCR methods are well known and are described, for example, in Innis *et al.*, eds., 1990, PCR Protocols: A Guide to Methods and Applications, Academic Press Inc. San Diego, CA. It will be apparent that computer controlled robotic systems are useful for isolating and amplifying nucleic acids.

25           An alternative means for generating the nucleic acid for the microarray is by synthesis of synthetic polynucleotides or oligonucleotides, *e.g.*, using N-phosphonate or phosphoramidite chemistries (Froehler *et al.*, Nucleic Acid Res. 1986, 14:5399-5407; McBride *et al.*, Tetrahedron Lett. 1983, 24:245-248). Synthetic sequences are between about 15 and about 500 bases in length, more typically between about 20 and about 50  
30 bases. In some embodiments, synthetic nucleic acids include non-natural bases, *e.g.*, inosine. As noted above, nucleic acid analogues may be used as binding sites for

hybridization. An example of a suitable nucleic acid analogue is peptide nucleic acid (see, for example, Egholm *et al.*, Nature 1993, 365:566-568. See, also, U.S. Patent No. 5,539,083).

In an alternative embodiment, the binding (hybridization) sites are made from  
5 plasmid or phage clones of genes, cDNAs (*e.g.*, expressed sequence tags), or inserts  
therefrom (Nguyen *et al.*, Genomics 1995, 29:207-209). In yet another embodiment, the  
polynucleotide of the binding sites is RNA.

*Attaching Nucleic Acids to the Solid Surface.* The nucleic acids or analogues are  
attached to a solid support, which may be made from glass, plastic (*e.g.*, polypropylene,  
10 nylon), polyacrylamide, nitrocellulose, or other materials. A preferred method for  
attaching the nucleic acids to a surface is by printing on glass plates, as is described  
generally by Schena *et al.*, Science 1995, 270:467-470. This method is especially useful  
for preparing microarrays of cDNA. See also DeRisi *et al.*, Nature Genetics 1996, 14:457-  
460; Shalon *et al.*, Genome Res. 1996, 6:639-645; and Schena *et al.*, Proc. Natl. Acad.  
15 Sci. USA 1995, 93:10539-11286.

A second preferred method for making microarrays is by making high-density  
oligonucleotide arrays. Techniques are known for producing arrays containing thousands  
of oligonucleotides complementary to defined sequences, at defined locations on a surface  
using photolithographic techniques for synthesis *in situ* (see, Fodor *et al.*, Science 1991,  
20 251:767-773; Pease *et al.*, Proc. Natl. Acad. Sci. USA 1994, 91:5022-5026; Lockhart *et al.*,  
Nature Biotech. 1996, 14:1675. See, also, U.S. Patent Nos. 5,578,832; 5,556,752;  
and 5,510,270) or other methods for rapid synthesis and deposition of defined  
oligonucleotides (Blanchard *et al.*, Biosensors & Bioelectronics 1996, 11:687-90). When  
these methods are used, oligonucleotides (*e.g.*, 20-mers) of known sequence are  
25 synthesized directly on a surface such as a derivatized glass slide. Usually, the array  
produced is redundant, with several oligonucleotide molecules per RNA. Oligonucleotide  
probes can be chosen to detect alternatively spliced mRNAs.

Other methods for making microarrays, *e.g.*, by masking (Maskos and Southern,  
Nuc. Acids Res. 1992, 20:1679-1684), may also be used. In principal, any type of array,  
30 for example, dot blots on a nylon hybridization membrane (see, Sambrook *et al.*, Molecular

Cloning—A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1989), could be used, although, as will be recognized by those of skill in the art, very small arrays will be preferred because hybridization volumes will be smaller.

5           **Generating Labeled Probes.** Methods for preparing total and poly(A)+ RNA are well known and are described generally in Sambrook *et al.*, *supra*. In one embodiment, RNA is extracted from cells of the various types of interest in this invention using guanidinium thiocyanate lysis followed by CsCl centrifugation (Chirgwin *et al.*, Biochemistry 1979, 18:5294-5299). Poly(A)+ RNA is selected by selection with oligo-dT  
10 cellulose (see Sambrook *et al.*, *supra*). Cells of interest may include, but are not limited to, wild-type cells, surrogate cells, drug-exposed wild-type cells, modified cells, and drug-exposed modified cells.

Labeled cDNA is prepared from mRNA by oligo dT-primed or random-primed reverse transcription, both of which are well known in the art (see, for example, Klug and  
15 Berger, Methods Enzymol. 1987, 152:316-325). Reverse transcription may be carried out in the presence of a dNTP conjugated to a detectable label, most preferably a fluorescently labeled dNTP. Alternatively, isolated mRNA can be converted to labeled antisense RNA synthesized by *in vitro* transcription of double-stranded cDNA in the presence of labeled dNTPs (Lockhart *et al.*, Nature Biotech. 1996, 14:1675). In alternative embodiments, the  
20 cDNA or RNA probe can be synthesized in the absence of detectable label and may be labeled subsequently, *e.g.*, by incorporating biotinylated dNTPs or rNTP, or some similar means (*e.g.*, photo-cross-linking a psoralen derivative of biotin to RNAs), followed by addition of labeled streptavidin (*e.g.*, phycoerythrin-conjugated streptavidin) or the equivalent.

25           When fluorescently-labeled probes are used, many suitable fluorophores are known, including fluorescein, lissamine, phycoerythrin, rhodamine (Perkin Elmer Cetus), Cy2, Cy3, Cy3.5, Cy5, Cy5.5, Cy7, FluorX (Amersham) and others (see, *e.g.*, Kricka, 1992, Nonisotopic DNA Probe Techniques, Academic Press San Diego, CA). It will be appreciated that pairs of fluorophores are chosen that have distinct emission spectra so that  
30 they can be easily distinguished.

In another embodiment, a label other than a fluorescent label is used. For example, a radioactive label, or a pair of radioactive labels with distinct emission spectra, can be used (see Zhao *et al.*, Gene 1995, 156:207; Pietu *et al.*, Genome Res. 1996, 6:492). However, because of scattering of radioactive particles, and the consequent requirement for widely spaced binding sites, use of radioisotopes is a less-preferred embodiment.

In one embodiment, labeled cDNA is synthesized by incubating a mixture containing 0.5 mM dGTP, dATP and dCTP plus 0.1 mM dTTP plus fluorescent deoxyribonucleotides (*e.g.*, 0.1 mM Rhodamine 110 UTP (Perkin Elmer Cetus) or 0.1 mM Cy3 dUTP (Amersham)) with reverse transcriptase (*e.g.*, SuperScript.TM. II, LTI Inc.) at 42 °C. for 60 minutes.

**Hybridization to Microarrays.** Nucleic acid hybridization and wash conditions are chosen so that the probe “specifically binds” or “specifically hybridizes” to a specific array site, *i.e.*, the probe hybridizes, duplexes or binds to a sequence array site with a complementary nucleic acid sequence but does not hybridize to a site with a non-complementary nucleic acid sequence. As used herein, one polynucleotide sequence is considered complementary to another when, if the shorter of the polynucleotides is less than or equal to 25 bases, there are no mismatches using standard base-pairing rules or, if the shorter of the polynucleotides is longer than 25 bases, there is no more than a 5% mismatch. Preferably, the polynucleotides are perfectly complementary (no mismatches). It can easily be demonstrated that specific hybridization conditions result in specific hybridization by carrying out a hybridization assay including negative controls (see, *e.g.*, Shalon *et al.*, *supra*; and Chee *et al.*, *supra*).

Optimal hybridization conditions will depend on the length (*e.g.*, oligomer versus polynucleotide greater than 200 bases) and type (*e.g.*, RNA, DNA, PNA) of labeled probe and immobilized polynucleotide or oligonucleotide. General parameters for specific (*i.e.*, stringent) hybridization conditions for nucleic acids are described above. When cDNA microarrays, such as those described by Schena *et al.* are used, typical hybridization conditions are hybridization in 5x SSC plus 0.2% SDS at 65 °C for 4 hours, followed by washes at 25° C in low stringency wash buffer (*e.g.*, 1x SSC plus 0.2% SDS) followed by 10 minutes at 25° C in high stringency wash buffer (0.1x SSC plus 0.2% SDS). See, Shena

*et al.*, Proc. Natl. Acad. Sci. USA 1996, 93:10614). Useful hybridization conditions are also provided in, *e.g.*, Tijessen, 1993, Hybridization With Nucleic Acid Probes, Elsevier Science Publishers B.V. See, also, Kricka, 1992, Nonisotopic DNA Probe Techniques, Academic Press, San Diego, CA.

- 5           **Signal Detection and Data Analysis.** When fluorescently labeled probes are used, the fluorescence emissions at each site of a transcript array can be preferably detected by scanning confocal laser microscopy. In one embodiment, a separate scan, using the appropriate excitation line, is carried out for each of the two fluorophores used. Alternatively, a laser can be used that allows simultaneous specimen illumination at
- 10 wavelengths specific to the two fluorophores and emissions from the two fluorophores can be analyzed simultaneously (see, Shalon *et al.*, Genome Research 1996, 6:639-645). In a preferred embodiment, the arrays are scanned with a laser fluorescent scanner with a computer controlled X-Y stage and a microscope objective. Sequential excitation of the two fluorophores is achieved with a multi-line, mixed gas laser and the emitted light is split
- 15 by wavelength and detected with two photomultiplier tubes. Fluorescence laser scanning devices are described in Schena *et al.*, Genome Res. 1996, 6:639-645 and in other references cited herein. Alternatively, the fiber-optic bundle described by Ferguson *et al.*, Nature Biotech. 1996, 14:1681-1684, may be used to monitor mRNA abundance levels at a large number of sites simultaneously.
- 20           Signals are recorded and, in a preferred embodiment, analyzed by computer, *e.g.*, using a 12 bit analog to digital board. In one embodiment the scanned image is despeckled using a graphics program (*e.g.*, Hijaak Graphics Suite) and then analyzed using an image gridding program that creates a spreadsheet of the average hybridization at each wavelength at each site. If necessary, an experimentally determined correction for "cross talk" (or
- 25 overlap) between the channels for the two fluors may be made. For any particular hybridization site on the transcript array, a ratio of the emission of the two fluorophores can be calculated. The ratio is independent of the absolute expression level of the cognate gene, but is useful for genes whose expression is significantly modulated, *e.g.*, by administering a drug, drug-candidate or other compound, or by any other tested event.

In one embodiment of the invention, the relative abundance of an mRNA in two cells or subjects or cell lines tested (*e.g.*, in a treated versus untreated cell or subject) may be scored as perturbed (*i.e.*, where the abundance is different in the two sources of mRNA tested) or as not perturbed (*i.e.*, where the relative abundance in the two sources is the same or is unchanged). Preferably, the difference is scored as perturbed if the difference between the two sources of RNA of at least a factor of about 10% (*i.e.*, RNA from one source is about 10% more abundant than in the other source), or may be about 25% or about 50%. Still more preferably, the RNA may be scored as perturbed when the difference between the two sources of RNA is at least about a factor of 1.5. Indeed, the difference in abundance between the two sources may be by a factor of two, of five, or more.

In other embodiments, it may be advantageous to also determine the magnitude of the perturbation. This may be done, as noted above, by calculating the ratio of the emission of the two fluorophores used for differential labeling, or by analogous methods that will be readily apparent to those of skill in the art.

In a specific embodiment, exemplified below, Affymetrix® Microarray Suite software can be employed for image acquisition and normalization of the fluorescent signals using internal standards. Analysis of the resultant signal intensities over each oligonucleotide, or data point, within each experiment may then fall into two main categories: supervised learning algorithms (Golub *et al.*, 1999; Slonim *et al.*, 1999; Yeang *et al.*, 2001; Ramaswamy *et al.*, 2001), and Hierarchical Clustering (Eisen *et al.*, 1998; Alizadeh *et al.*, 2000; Perou *et al.*, 2000) (see Example A for the full reference citations). Preferably any algorithms to be employed have the capacity to analyze the very large data-sets, and allow comparisons of multiple experiments and multiple points within a single experiment, for determining expression profiles.

### EXAMPLES

The following Example(s) illustrate the invention, but are not limiting.

## EXAMPLE 1: EXPRESSION PROFILING OF BLOOD CELLS DISTINGUISHES PROSTATE CANCER PATIENTS

### Patient and Control Subject Recruitment and Study Procedure

Institutional Review Board (IRB) approval of the study protocol was obtained.

- 5        **Medical Exclusions.** A list of medical exclusions was generated for both prostate cancer patients and control subjects. A blood count (CBC) was performed for all samples collected and subjects were excluded if their cell counts were outside of the normal range. Serum PSA tests were performed on all patient and control subjects. Any control subject with serum PSA > 4ng/ml was excluded from further analysis (n=0).
- 10        **Prostate Cancer Subjects.** Eleven subjects have been recruited for this study since the initiation of screening of men undergoing radical prostatectomy for treatment of prostate cancer. For all subjects, informed consent was obtained according to the regulations of the IRB. Subjects completed a questionnaire (with the assistance of the study coordinator), documenting current medication and general health status. Fifteen ml of blood was then
- 15        drawn prior to surgery for prostate removal. Blood was processed immediately as described below. All patient records were screened and pertinent data entered into the subject database, such as serum PSA values (at the time of surgery, prior to surgery, and post surgery), date of biopsy, Gleason score at biopsy and post prostatectomy, TNM tumor stage. The IRB approved study protocol allows the study team to access all patient records
- 20        following surgery. Ethnicity of prostate cancer subjects was as follows: Caucasian = 5, Hispanic = 3, African American = 2, Asian = 1.

- 25        **Control Subjects.** Seven control subjects, age-matched to the patient group, were recruited. Subjects completed a questionnaire documenting that neither they nor their first degree relatives had a history of prostate cancer, or any other tumor. Questionnaires were also completed listing current medication use and medical history. Subjects were seen at
- 30        their place of work and an informed consent interview was conducted and consent obtained according to the regulations of the IRB. 15ml blood was drawn from each control and processed immediately as described below. 3ml blood was employed for PSA and CBC tests, 12ml was employed for leukocyte extraction. Ethnicity of age-matched control
- 30        subjects was as follows: Caucasian = 4, Hispanic = 2, African American = 1, Asian = 0.



***Sample Processing and Microarray Hybridization.*** Immediately after collection, blood leukocytes were isolated by lysis of red cells, centrifugation and washing, according to standard protocols (Qiagen). Total purified leukocytes were split into two tubes and stored at -70° C prior to RNA extraction. In studies performed for other projects it is possible to store leukocyte samples for up to 6 months with no effect to quality or quantity of the RNA extracted. Total RNA was extracted in duplicate from the two leukocytes samples, using an RNA preparation kit and accompanying protocol (Qiagen). RNA was quantified by UV spectrometry, using RNA standards for normalization. The quality of RNA was analyzed by electrophoresis through formaldehyde agarose gels. Only RNA samples with good quality ribosomal RNA were processed to completion. For samples employed for microarray analysis, 8 µg of total RNA was used as a template for cDNA synthesis, using an oligo-dT primer and Reverse Transcriptase enzyme, according to standard Affymetrix protocols. Purified cDNA was then employed as a template to generate biotin labeled cRNA, using Enzo Bioarray High Yield RNA Transcript labeling Kits (Enzo). cRNA samples were quantified and stored at -70° C prior to fragmentation and hybridization.

Following fragmentation of the cRNA samples, 20ng of each fragmented product was hybridized to an Affymetrix TEST3 array to check the quality of each sample. In each instance the cRNA sample was then hybridized to an HU95A GeneChip array. Patient and control samples were processed and hybridized in a random order.

***Affymetrix® Microarray Suite Software.*** Following scanning of GeneChip arrays, data acquisition of each array was performed using the Affymetrix Microarray Software Suite V5. Briefly, this software initially quantifies the signal over every oligonucleotide probe set on the microarray, then normalizes against the intensity of the signal over the internal control oligonucleotides. The probe set for each gene is then queried by perfect match (PM) and mismatch (MM) oligonucleotide probes, each 25 bases in length. The MM probes have a single base change in the center of the oligonucleotide sequence. Comparison of the hybridization signals from the PM and MM probes permits a measurement of the specificity of signal intensity, and eliminates from the data analysis the majority of non-specific cross hybridization. Values of intensity difference, as well as ratios of each probe pair, are used to determine whether a gene is “present”, *i.e.* the

sample that was hybridized to the array expresses that genes transcript, or “absent”- there is no expression of that gene in the sample used for RNA extraction. To normalize between arrays (to remove experimental noise, such as differences in final cRNA quantity), each array was scaled using a target intensity of 100.

5           The resultant data was converted to Excel spreadsheets, and collated. As described above, each sample was processed in duplicate. Therefore all data analysis was performed on both the original expression values for each subject duplicate sample, plus the mean expression values of the duplicate subject samples. All gene expression values that were given an “absent call” were removed from the data sets. Gene expression data was filtered  
10 by removing all genes with expression levels less than two standard deviation above background levels. All statistical tests and data analysis were performed in Excel, except those described in detail below.

*Data analysis; Hierarchical Clustering.* Following normalization and filtering, unsupervised and supervised hierarchical clustering was performed using the Cluster  
15 program (M.Eisen, discussed Example A). The gene expression data was log-transformed and then median centered over each patient and control sample. Log intensity values for each gene (row), within each subject (column), were then normalized to set all the magnitudes (sum of the squares of the values) to 1.0. Average-linked clustering was performed on this adjusted dataset, employing a correlation centered metric. In this  
20 experiment, all genes and subjects were given an equal weighting of 1.0. The results of the clustering run were visualized using the program TreeView (M.Eisen).

*Real-Time Polymerase Chain Reaction.* 200ng of total RNA from all patients and controls was employed for first strand cDNA synthesis, using random hexamer primers and Superscript<sup>II</sup> Reverse Transcriptase enzyme (Invitrogen). Primers were designed using the  
25 Primer3 program (Whitehead Institute), except for the 18S ribosomal RNA primers, which were purchased as an internal standard PCR kit (Ambion). For real-time PCR the SYBR Green assay, which measures the linear binding of florescent molecules to double-stranded DNA at each cycle of the PCR amplification, was performed using the Quantitech Kit (Qiagen), on an ABI PRISM 7700 apparatus. The resultant florescence data was imported  
30 into Sequence Detector, v1.7a software (ABI), and Cts were calculated. The Ct (the PCR

threshold cycle where an increase in reporter fluorescence above a baseline signal can first be detected) has a direct correlation with template concentration. The Cts of samples with known copy numbers were employed to generate standard amplification curves for each set of specific gene primers. Final copy numbers of each patient and control RNA sample were determined from each standard curve, and compared with the control 18S standard results.

Standard PCR protocols were also employed to analyze genes expressed at very low levels in subject leukocytes. cDNA was prepared as described above, and then employed as a template for PCR, using Hotstar polymerase enzyme (Qiagen) and a Hybaid PCR apparatus. Products were analyzed by staining with ethidium bromide following agarose gel electrophoresis. DNA was visualized using a gel documentation system (Kodak).

### **Results of the Preliminary Studies**

***Pair-wise Analysis of Microarray Results.*** To investigate total sample variability, a pair-wise comparison of expression levels was performed. It is expected that over 12,000 data points, samples should be highly correlated to allow meaningful comparison of the data. Correlation coefficients were within the range of 0.85-0.93 for each comparison (data not shown). In preliminary studies duplicate processing was performed, and pair-wise comparisons between duplicates showed high correlations between intra-subject samples. A scatter plot of expression data from patient A (sample A1-0 and A1-2) yielded an  $R^2$  value of 0.967.

***Analysis of gene expression from genes differentially regulated in peripheral blood.*** Expression level data for each of the genes previously found to be differentially regulated in peripheral blood were investigated. The mean expression levels were calculated across subjects processed to date from the two groups (mean expression values over duplicate samples). Decreased levels of *MSH2* were observed (>20% lower in patients than controls), which although is not significantly different between subject groups ( $p > 0.05$ ), is consistent with the findings reported by Strom *et al.* (Strom *et al.*, Prostate 2001;47(4):269-75). Additionally, it was found that transcript levels of IFN gamma were decreased by >20% in the patient leukocytes compared to control subjects. Decreasing levels of serum IFN gamma protein were previously found to correlate with increasing

tumor mass (Elsasser-Beile *et al.*, J Cancer Res Clin Oncol. 1993; 119(7):430-3), and the present data suggests that this correlation is directly related to decreased expression in patient peripheral blood leukocytes.

Of interest to this Example 4 in this invention, transcript levels of *HER2* were found to be increased in the blood of prostate cancer patients when compared to control subjects (>38% increased in patients versus control subjects). *HER2*, a proto-oncogenic member of the type 1 tyrosine kinase family is amplified in up to 30% of human breast cancers (Slamon *et al.*, Science. 1987;9;235(4785):177-82), and serum levels of *HER2*, plus RT-PCR amplification of *HER2* from circulating metastatic breast cancer cells are being explored as predictors of breast cancer patient survival (Willsher *et al.*, Breast Cancer Res Treat. 1996; 40(3):251-5). Furthermore, many genes that were found to be altered to a much larger degree between the two subject groups than the genes described above, validating the experimental design of using a microarray approach to identify patterns of differentially regulated genes. Examples include the genes *Megakaryocyte associated tyrosine kinase* (116% decreased in patients versus controls, or > 3 fold decrease), programmed cell death-like cDNA (72% decreased in patients versus controls, or >2.8 fold decrease) and *MMP9* (40% increased in patients versus controls, or >2 fold increase).

***Analysis of IL-8 Leukocyte Gene expression.*** Veltri *et al.*, *supra*, reported a significant increase in *IL-8* gene expression in leukocytes from patients with metastatic disease, when compared to *IL-8* transcript levels from a pool of control subjects. Analysis of expression levels following microarray hybridization of cRNA transcribed from each patient and control sample showed that *IL-8* expression, although quite low, was not different between the two subject groups. The microarray *IL-8* gene expression was investigated further, using a PCR based approach. cDNA was transcribed from each RNA sample, , and then employed in a real-time PCR assay. To standardize input cDNA and thus RNA levels, PCR amplification products were normalized to the 18S ribosomal RNA gene. Thus real-time PCR was performed, employing 18S primers at concentrations that have been optimized to be in the range of amplification consistent with genes expressed at low levels (Ambion).

***Real-Time PCR of the 18S Ribosomal RNA gene.*** The normalized SYBR Green signal (log Rn; Y axis) is plotted against PCR cycle number (X axis) for each sample. In this experiment, an arbitrary Ct was set to intersect each sample within the linear amplification stage of the PCR, and is represented by the dotted horizontal line. The samples show the control amplifications of a known sample concentration, at no dilution (1.0), 10 fold dilution, 100 fold and 1000 fold. Six subject sample 18S PCR amplifications are performed in duplicate.

A standard curve for 18S was generated, using dilutions of the control sample. The standard curve can be employed to determine both the relative concentration of starting template in each of the subject samples, as well as the actual numbers of molecules employed for analysis. The Cts calculated for each of the subject samples by the Sequence Detector, v1.7a software (ABI), were thus employed to determine the concentration of starting template for each of the samples which were found to be consistent with each other.

In the *IL-8* assay, no DNA product was detected in any of the samples after 25 cycles of amplification (which is similar to PCR protocols followed by Veltri *et al.*, Urology 1999; 53(1):139-47). After 40 PCR cycles, product was observed with a clear difference in *IL-8* amplification was detected among the samples (data not shown). In each instance, levels of amplification were correlated with those detected following microarray hybridization described above. These results suggest that *IL-8* expression is not a marker of localized prostate cancer, but increased expression levels of *IL-8* may be a marker of metastatic disease, as detected by Veltri *et al.* (Veltri *et al.*, *supra*).

***Hierarchical Clustering of Prostate Cancer Patients and Control Subjects.***

Following normalization and filtering of the data, an unsupervised hierarchical clustering was initially performed, where data is analyzed in the Cluster program, with no previous set constraints on the data. For this analysis, the gene expression data was log transformed and then median centered over each patient and control sample. Following filtering of the data, an initial analysis of genes found to be called "present" in at least two of the samples processed to date was performed; thus a total of 6834 genes remained for further investigation. An unsupervised hierarchical clustering algorithm was implemented, employing the expression intensity levels of genes from 18 subjects. An average-linked

cluster was performed on both absolute intensity values of each sample ( $n=18 \times 2$ ), and the mean intensity levels over the duplicate samples ( $n=18$ ). Results from both Cluster analysis were viewed in the TreeView program (data not shown), and indicated that using the expression level measurements of 6834 genes, 90% of the prostate cancer patients clustered into one node. However, the classification was not exact as two control subjects also clustered into this node (data not shown).

***Supervised Hierarchical Clustering Prostate Cancer Patients and Control Subjects.***

It may prove useful to perform a supervised clustering experiment, as surrogate tissue in which differences in the patterns of gene expression of leukocytes from tumor patients may be more subtle than the differences obtained from analysis of the tumor tissue itself. Other researchers investigating diagnostic gene expression profiles have performed supervised clustering by manipulating the data before input into the algorithm, for example Dhanasekaran *et al.* computed t-statistics of prostate cancer versus benign sample for each gene, to create a more limited and also more informative set of genes for analysis (Dhanasekaran *et al.*, Nature. 2001; 412(6849):822-6.). Following this example a student two-tailed t-test across the 6834 genes expressed in the patient and control subjects leukocytes was performed. Of the original 6834 genes, 896 were found to have expression values significantly different between the patients and controls ( $p < 0.05$ ), and 1535 were found to have  $p < 0.1$  between the two groups. Also performed was an identical student T-test on different permutations of randomized data, where subject samples were randomly placed into one of the two groups (using an approach similar to a permutation method for analysis of non-random data; Draghici *et al.*, Drug Discov Today 2002; 7(11):S55-S63). It was found that the average number of genes found to be significantly different between the randomized groups was 200 ( $p < 0.05$ ), while  $< 500$  genes were found to have  $p < 0.1$ . A t-test performed on the p-values of the "real" group versus the random groups showed a significant difference between groups ( $p < 0.0001$ ). Therefore, randomizing the data results in nearly 80% less genes found to be significantly different between subject groups and may represent the noise of this experimental system.

***TreeView Representation of Cluster patterns of gene expression among men with prostate cancer and age-matched control subjects (Figure 1).*** Data are represented in matrix format. Each row represents a single gene (for space gene names have been

omitted). Each column represents an experimental leukocyte patient or control sample. For each sample the ratio of the abundance of transcripts of each gene, to the median abundance of the genes's transcript among the individuals leukocytes, is represented by the color of the corresponding matrix. Green means that transcript levels are less than median; black means the transcript levels are median; red means the transcript levels are greater than median. Grey is used to indicate that the gene is absent. Color saturation represents the magnitude of the ratio relative to the median for the total set of samples. A dendrogram along the horizontal axis indicates the clusters of most similar subjects, based on gene expression levels of 1535 genes. The dendrogram along the vertical axis represents sample nodes of the total Cluster results, where genes appear together on the branches of the tree if they have similar patterns of gene expression. Examples of Cluster nodes are taken from the total TreeView data, showing genes that are generally expressed at lower levels in the prostate cancer samples (A1 to A13), than control subject samples (B1 to B7). A scaled representation of the horizontal dendrogram showing patient and control cluster results can be shown.

The 1535 genes ( $p < 0.1$ ) were further analyzed employing the Cluster program with readout in TreeView. Again, this analysis was performed using both the mean of duplicate subject samples and the absolute intensity levels of each sample. Figure 1 shows an example of this data analysis, where mean intensity levels were employed for all but three samples. The results of this supervised cluster analysis indicates that the overall leukocyte expression of 1535 genes from the 11 prostate cancer patients is different to the overall gene expression data of the seven control subjects. Specifically, the prostate cancer patients cluster in a node that is separate to the node of control subjects, and suggests that distinctive patterns of gene expression can be employed to differentiate between prostate cancer patients and control subjects. The use of duplicate samples permits a finding that experimental difference (as observed between B2-0 and B2-1), do not influence the final cluster results.

To perform an investigation on this clustering result, subject gene expression levels were randomized within the dataset and the resultant data were re-clustered. Five different re-iterations of randomizing the data were performed. A TreeView readout from the clustering of 1535 genes, where subjects have been classified into one of two nodes

representing cancer patients or control subjects, and a TreeView readout generated following Cluster analysis of the randomized dataset was used to analyze the data (Figure 2). Short branch lengths between each node of the dendrogram of random data show that following intra-subject randomization, patient samples have overall gene expression patterns very similar to each other. Furthermore, the dendrogram has not organized the samples into an order significantly different from the initial order of data input into the Cluster algorithm and duplicate samples are dispersed over the tree. The Cluster analysis of the other random data iterations resulted in TreeView readouts where either the samples remained in the order of input into Cluster, or alternatively branch lengths were observed to be vastly reduced, indicating very minor differences in overall gene expression between subjects. These results suggest that this supervised hierarchical clustering, which demonstrates a correct classification of prostate cancer patients and control subjects into their respective groups, is not due to random microarray data.

Table 1 shows a list of genes from PBLs up- or down-regulated in prostate cancer subjects.

*Table 1. Prostate Cancer Gene Expression Results*

This table includes gene expression profile data from 11 prostate cancer patients versus 6 control subjects. The table includes the Affymetrix probe-set ID for the HU95Av2 GeneChip array, and also the EASE assignment. The EASE data were included because there are instances where an unknown EST (as referenced to by the Affymetrix probeset ID) has later been characterized by others. However, these curation methods are not 100% accurate.

It is very important to note that the significance levels for the genes/ESTs can change with increasing statistical power from comparing additional samples. Therefore, it may be likely that some genes/ESTs may change in significance.

Affymetrix HU95A version2 probe set ids	Mean levels expression in prostate cancer patients compared to healthy controls	two tailed Students t-test significance	EASE Names ( <a href="http://david.niaid.nih.gov/david/ease.html">david.niaid.nih.gov/david/ease.html</a> )
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37046_at	down	1.95E-07	proteasome (prosome, macropain) subunit, alpha type, 5
2010_at	down	3.1E-07	S-phase kinase-associated protein 1A (p19A)
36546_r_at	up	1.66E-06	KIAA0542 gene product
33602_at	up	4.77E-06	endothelial differentiation, G-protein-coupled receptor 6
36591_at	up	4.9E-06	tubulin, alpha 1 (testis specific)
33190_g_at	up	5.31E-06	chromosome 10 open reading frame 6
32595_at	down	6.5E-06	G-rich RNA sequence binding factor 1
39030_at	up	7.14E-06	Rab acceptor 1 (prenylated)
36567_at	up	7.59E-06	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7
32066_g_at	up	9.85E-06	cAMP responsive element modulator
38964_r_at	up	1.15E-05	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
35485_at	up	1.35E-05	glutamate receptor, metabotropic 4
32622_at	up	1.53E-05	dynamitin 2
33126_at	down	1.7E-05	glycosyltransferase AD-017
38621_at	up	1.9E-05	dimethylarginine dimethylaminohydrolase 2
31620_at	up	2.07E-05	similar to transcription factor TBX10
330_s_at	up	2.28E-05	Tubulin, Alpha 1, Isoform 44
32378_at	up	2.76E-05	pyruvate kinase, muscle
36098_at	down	2.87E-05	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
1268_at	up	3.43E-05	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)
31391_at	up	6.24E-05	huntingtin-associated protein 1 (neuroan 1)
39797_at	down	6.39E-05	ubiquitin ligase E3 alpha-II
1660_at	down	6.4E-05	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)
31901_at	up	7.3E-05	potassium voltage-gated channel, shaker-related subfamily, beta member 2
1772_s_at	down	7.48E-05	farnesyltransferase, CAAX box, alpha
36994_at	up	8.05E-05	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
32659_at	down	8.47E-05	eukaryotic translation Initiation factor 2B, subunit 4 delta, 67kDa
41248_at	down	9.53E-05	likely ortholog of mouse variant polyadenylation protein CSTF-64
39709_at	up	0.000116	selenoprotein W, 1
31740_s_at	up	0.000125	paired box gene 4
40418_at	down	0.000125	retinoblastoma binding protein 4
39792_at	down	0.000141	heterogeneous nuclear ribonucleoprotein R
41078_at	up	0.000149	KIAA0150 protein
31341_at	up	0.000154	potassium voltage-gated channel, Shaw-related subfamily, member 3

32163_f_at	up	0.000157	chorionic somatomammotropin hormone 2
676_g_at	up	0.000162	interferon induced transmembrane protein 1 (9-27)
34832_s_at	up	0.000163	KIAA0763 gene product
924_s_at	down	0.000166	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
34491_at	up	0.000166	2'-5'-oligoadenylate synthetase-like
1392_at	up	0.000172	G protein-coupled receptor kinase 6
39118_at	down	0.000176	DnaJ (Hsp40) homolog, subfamily A, member 1
34141_at	up	0.000188	
31785_f_at	up	0.000197	unnamed HERV-H protein
41219_at	down	0.000227	KIAA0570 gene product
38105_at	down	0.000234	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4
37334_at	down	0.000239	heterogeneous nuclear ribonucleoprotein A0
40452_at	up	0.000249	copine I
32784_at	down	0.000259	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
31968_at	up	0.000266	
36907_at	up	0.000271	mevalonate kinase (mevalonic aciduria)
35577_at	up	0.000275	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7
32115_r_at	up	0.000285	adenosine A2a receptor
1577_at	up	0.000288	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
1830_s_at	up	0.000295	transforming growth factor, beta 1 (Camurati-Engelmann disease)
33803_at	down	0.000306	thrombomodulin
41159_at	down	0.000311	clathrin, heavy polypeptide (Hc)
1158_s_at	up	0.000315	calmodulin 3 (phosphorylase kinase, delta)
39162_at	down	0.000328	Arg/Abl-interacting protein ArgBP2
37201_at	up	0.000335	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)
37383_f_at	up	0.000338	major histocompatibility complex, class I, C
41836_at	down	0.000345	calcium homeostasis endoplasmic reticulum protein
38963_i_at	up	0.000349	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
34827_at	up	0.000362	unc-51-like kinase 1 (C. elegans)
37074_at	up	0.00037	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)
37746_r_at	up	0.000372	suppression of tumorigenicity 5
37267_at	up	0.000373	thimet oligopeptidase 1
33779_at	up	0.000386	vesicle-associated membrane protein 1 (synaptobrevin 1)
457_s_at	down	0.000395	ubiquitin-like 1 (sentrin)

41745_at	up	0.000404	interferon induced transmembrane protein 3 (1-8U)
37468_at	down	0.000419	Janus kinase 2 (a protein tyrosine kinase)
35802_at	down	0.000424	formin binding protein 4
1696_at	down	0.000429	polymerase (DNA directed), beta
38409_at	down	0.000433	sperm specific antigen 2
38093_at	down	0.000442	chromosome 14 open reading frame 32
36143_at	down	0.000469	caspase 3, apoptosis-related cysteine protease
34151_at	up	0.000471	DKFZP586M1019 protein
41033_at	down	0.000475	zinc finger protein 84 (HPF2)
32053_at	down	0.000477	cyclin T2
38865_at	up	0.000509	GRB2-related adaptor protein 2
36377_at	up	0.00052	interleukin 18 receptor 1
37977_at	up	0.00052	deltex homolog 2 (Drosophila)
32447_at	up	0.000538	nuclear receptor subfamily 5, group A, member 1
36926_at	down	0.00055	mitogen-activated protein kinase 6
869_at	down	0.000554	general transcription factor IIA, 2, 12kDa
34604_at	up	0.000585	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4
41795_at	down	0.000605	NCK adaptor protein 1
33542_at	up	0.00061	
40355_at	up	0.000621	AND-1 protein
40585_at	down	0.000638	adenylate cyclase 7
34384_at	down	0.000654	ATP-binding cassette, sub-family C (CFTR/MRP), member 1
34907_at	up	0.000654	apoptosis-associated tyrosine kinase
2058_s_at	up	0.000655	integrin, beta 5
35899_at	up	0.000659	artemin
140_s_at	down	0.000663	splicing factor, arginine/serine-rich 10 (transformer 2 . homolog, Drosophila)
40976_at	up	0.000674	katanin p80 (WD repeat containing) subunit B 1
33180_at	down	0.000681	protein phosphatase 1, regulatory (inhibitor) subunit 2
34157_f_at	up	0.000685	histone 1, H2a1
32080_at	up	0.000692	tetracycline transporter-like protein
39336_at	up	0.000697	ADP-ribosylation factor 3
36675_r_at	up	0.000703	profilin 1
36720_at	up	0.000705	pyruvate dehydrogenase kinase, isoenzyme 3
38223_at	down	0.000723	TBC1 domain family, member 8 (with GRAM domain)
32198_at	up	0.000738	hypothetical protein FLJ20452
40007_at	up	0.000744	zinc finger protein, subfamily 1A, 1 (Ikaros)
1351_at	up	0.000757	EphB4
1307_at	down	0.000757	xeroderma pigmentosum, complementation group A
36258_at	up	0.000769	protein kinase, cGMP-dependent, type I
37692_at	down	0.000799	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)
32548_at	down	0.000801	inactive progesterone receptor, 23 kD
38608_at	up	0.000802	lectin, galactoside-binding, soluble, 7 (galectin 7)
37968_at	up	0.000806	natural cytotoxicity triggering receptor 3

39091_at	down	0.000806	vitamin A responsive; cytoskeleton related
39057_at	up	0.000808	kinesin 2 60/70kDa
33226_at	up	0.00082	KIAA0876 protein
40580_r_at	up	0.000825	parathymosin
41428_at	up	0.000843	ATP-binding cassette, sub-family C (CFTR/MRP), member 5
354_s_at	down	0.000847	RecQ protein-like (DNA helicase Q1-like)
34694_at	up	0.000848	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
32433_at	down	0.00085	
34098_f_at	up	0.000893	integrin cytoplasmic domain-associated protein 1
34062_at	up	0.000902	ets variant gene 2
38967_at	down	0.000913	chromosome 14 open reading frame 2
34330_at	down	0.000915	cytochrome c oxidase subunit VIIa polypeptide 2 like
32201_at	up	0.000925	Sjogren's syndrome nuclear autoantigen 1
1127_at	up	0.000936	ribosomal protein S6 kinase, 90kDa, polypeptide 1
40268_at	up	0.000942	FOS-like antigen 2
36023_at	down	0.000951	proline-rich protein HaeIII subfamily 1
AFFX-CreX-3_st	up	0.000965	
33913_at	up	0.000995	HLA-B associated transcript 2
37838_at	up	0.001007	coagulation factor XII (Hageman factor)
37098_at	up	0.001029	protoporphyrinogen oxidase
1333_f_at	up	0.001043	breakpoint cluster region
32904_at	up	0.001057	perforin 1 (pore forming protein)
33103_s_at	down	0.001068	adducin 3 (gamma)
34811_at	down	0.001072	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
40504_at	up	0.001073	paraoxonase 2
33764_at	up	0.001075	G protein-coupled receptor 51
35626_at	up	0.001085	N-sulfoglucosamine sulfohydrolase (sulfamidase)
38726_at	up	0.001085	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit
1794_at	up	0.001089	cyclin D3
534_s_at	up	0.001117	folate receptor 1 (adult)
34714_at	down	0.001123	SAM domain and HD domain 1
1452_at	down	0.001145	LIM domain only 4
35132_at	up	0.001152	myosin IF
40947_at	up	0.001185	hypothetical protein FLJ12671
36343_at	up	0.001189	tolloid-like 2
35693_at	up	0.001227	hippocalcin-like 1
34486_at	up	0.001262	
34702_f_at	up	0.001285	chorionic somatomammotropin hormone 2
35171_at	down	0.00129	spastic paraplegia 4 (autosomal dominant; spastin)
38057_at	up	0.001298	dermatopontin
41333_at	down	0.001302	centaurin, beta 2

34703_f_at	up	0.001305	chorionic somatomammotropin hormone 2
41821_at	down	0.001307	cell division cycle 2-like 5 (cholinesterase-related cell division controller)
41788_i_at	down	0.001308	KIAA0669 gene product
37604_at	down	0.001315	histamine N-methyltransferase
921_s_at	up	0.001335	
39444_at	down	0.001337	splicing factor 3b, subunit 1, 155kDa
38072_at	down	0.001339	hypothetical protein dJ465N24.2.1
39624_at	up	0.001377	leukotriene B4 receptor
AFFX- HSAC07/X00351 _M_at	up	0.001382	actin, beta
38449_at	up	0.0014	WD repeat domain 23
39353_at	down	0.001411	heat shock 10kDa protein 1 (chaperonin 10)
40260_g_at	up	0.001416	RNA binding motif protein 9
33372_at	up	0.001431	RAB31, member RAS oncogene family
39166_s_at	up	0.001476	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1
40138_at	up	0.00148	COP9 subunit 6 (MOV34 homolog, 34 kD)
35451_s_at	up	0.001495	SCAN domain containing 2
34802_at	up	0.001519	collagen, type VI, alpha 2
36654_s_at	down	0.00153	heterogeneous nuclear ribonucleoprotein A2/B1
33887_at	up	0.00159	hepatocyte growth factor-regulated tyrosine kinase substrate
39748_at	down	0.001591	
35753_at	up	0.001648	PRP8 pre-mRNA processing factor 8 homolog (yeast)
41752_at	down	0.001662	growth hormone inducible transmembrane protein
31926_at	up	0.001667	cytochrome P450, family 7, subfamily A, polypeptide 1
32407_f_at	up	0.001671	
39909_g_at	up	0.001683	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa
36270_at	down	0.001685	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)
40359_at	up	0.001688	chromosome 11 open reading frame 13
39079_at	down	0.001696	enhancer of rudimentary homolog (Drosophila)
650_s_at	down	0.001755	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
33783_at	up	0.001762	plexin B1
39119_s_at	up	0.001784	natural killer cell transcript 4
36814_at	down	0.001798	hypothetical protein KIAA1109
40518_at	down	0.001806	protein tyrosine phosphatase, receptor type, C

34056_g_at	up	0.001806	activin A receptor, type IB
40110_at	down	0.001822	isocitrate dehydrogenase 3 (NAD+) beta
421_at	up	0.001832	translocated promoter region (to activated MET oncogene)
37386_i_at	up	0.001833	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1
32803_at	down	0.001853	cornichon homolog (Drosophila)
38336_at	up	0.001856	GRP1-binding protein GRSP1
34263_s_at	down	0.001864	diaphanous homolog 2 (Drosophila)
39949_at	up	0.001866	molybdenum cofactor synthesis 1
36715_at	up	0.001899	adrenergic, alpha-1A-, receptor
38500_at	down	0.001906	CGI-109 protein
31557_at	up	0.001915	thymosin, beta 4, X chromosome
32206_at	up	0.001916	CDC42 binding protein kinase alpha (DMPK-like)
34819_at	down	0.001946	CD164 antigen, sialomucin
40988_at	down	0.001949	YME1-like 1 (S. cerevisiae)
38982_at	down	0.001952	telomeric repeat binding factor 2, interacting protein
31610_at	up	0.001954	membrane-associated protein 17
33378_at	down	0.001956	IDN3 protein
34353_at	down	0.00196	KIAA0648 protein
41529_g_at	down	0.001972	
36895_at	down	0.001975	origin recognition complex, subunit 3-like (yeast)
38814_at	down	0.001995	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit C isoform 1
35986_at	up	0.001998	MYST histone acetyltransferase 1
37075_at	up	0.002003	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)
37358_at	down	0.002024	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
37995_s_at	down	0.002036	fragile X mental retardation 1
36694_at	up	0.00204	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3
35804_at	down	0.002047	ash2 (absent, small, or homeotic)-like (Drosophila)
34409_at	up	0.002066	low density lipoprotein receptor-related protein 10
40360_at	up	0.002068	Protein P3
35600_at	down	0.00209	ROD1 regulator of differentiation 1 (S. pombe)
32005_at	up	0.002111	pro-melanin-concentrating hormone
40489_at	up	0.002142	dentatorubral-pallidolusian atrophy (atrophin-1)
38355_at	down	0.002155	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome
41598_at	down	0.002175	SEC22 vesicle trafficking protein-like 1 (S. cerevisiae)
193_at	down	0.002179	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
41756_at	down	0.002228	XPA binding protein 1
40509_at	down	0.00226	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)
36981_at	down	0.002271	signal recognition particle 9kDa

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40698_at	down	0.002275	mago-nashi homolog, proliferation-associated (Drosophila)
33664_g_at	up	0.002278	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)
37389_at	down	0.002286	small acidic protein
640_at	up	0.002306	angiotensin II receptor-like 2
37031_at	down	0.002324	chromosome 9 open reading frame 10
40844_at	down	0.00233	SH2 domain binding protein 1 (tetratricopeptide repeat containing)
35735_at	down	0.002374	guanylate binding protein 1, interferon-inducible, 67kDa
254_at	down	0.002379	H3 histone, family 3A
32232_at	down	0.002401	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa
39039_s_at	down	0.002472	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
35768_at	up	0.002473	ring finger protein 40
37145_at	up	0.002506	granulysin
41360_at	down	0.002506	CCR4-NOT transcription complex, subunit 8
1798_at	down	0.002559	LIV-1 protein, estrogen regulated
322_at	up	0.002593	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)
35035_at	up	0.002603	cholinergic receptor, nicotinic, beta polypeptide 3
34558_at	up	0.002611	opiate receptor-like 1
32789_at	down	0.002639	nuclear cap binding protein subunit 2, 20kDa
32422_at	up	0.002657	double C2-like domains, beta
31388_at	up	0.002677	early lymphoid activation protein
38880_at	up	0.002701	likely ortholog of mouse mitogen activated protein kinase binding protein 1
34611_at	up	0.002705	zinc finger protein 192
39629_at	up	0.002729	phospholipase A2, group V
1827_s_at	up	0.002732	v-myc myelocytomatosis viral oncogene homolog (avian)
34786_at	down	0.002751	jumonji domain containing 1
652_g_at	down	0.002754	replication protein A3, 14kDa
38480_s_at	up	0.002774	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)
38860_at	up	0.002779	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)
39083_at	down	0.002817	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
38589_l_at	down	0.00284	prothymosin, alpha (gene sequence 28)
38753_at	down	0.002847	exportin, tRNA (nuclear export receptor for tRNAs)
41423_at	up	0.002861	calsynenin 3
36474_at	down	0.002868	KIAA0776 protein
34336_at	down	0.00288	lysyl-tRNA synthetase
184_at	up	0.002913	angiotensin II receptor-like 1
33546_at	up	0.002927	

40044_at	up	0.002937	ELL gene (11-19 lysine-rich leukemia gene)
2031_s_at	up	0.002964	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
34178_at	up	0.002967	zinc finger protein 297
33098_at	down	0.003008	chemokine (C-C motif) receptor 3
955_at	up	0.003035	Calmodulin Type 1
33440_at	down	0.00306	transcription factor 8 (represses interleukin 2 expression)
31870_at	up	0.003092	CD37 antigen
31861_at	up	0.003094	immunoglobulin mu binding protein 2
36949_at	up	0.00313	casein kinase 1, delta
35681_r_at	down	0.003133	zinc finger homeobox 1b
1848_at	down	0.003145	RAP1A, member of RAS oncogene family
41612_at	up	0.003146	zinc finger protein 264
40038_at	up	0.003148	suppression of tumorigenicity 7
35749_at	up	0.003152	transcriptional adaptor 3 (NGG1 homolog, yeast)-like
38370_at	down	0.00316	
33848_r_at	down	0.003175	cyclin-dependent kinase inhibitor 1B (p27, Kip1)
35426_at	up	0.003201	SPPL2b
33417_at	up	0.003215	RAB3 GTPase-ACTIVATING PROTEIN
36791_g_at	up	0.003221	tropomyosin 1 (alpha)
38822_at	up	0.003235	serine/threonine kinase 17a (apoptosis-inducing)
40481_r_at	up	0.003244	FYN oncogene related to SRC, FGR, YES
36805_s_at	up	0.003265	neurotrophic tyrosine kinase, receptor, type 1
31519_f_at	down	0.003267	basic transcription factor 3, like 3
37844_at	down	0.003277	class I cytokine receptor
39553_at	down	0.003292	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
41386_i_at	up	0.003297	KIAA0346 protein
41141_at	down	0.003301	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)
40957_at	down	0.003302	joined to JAZF1
33820_g_at	down	0.00335	lactate dehydrogenase B
36688_at	down	0.003368	sterol carrier protein 2
1760_s_at	up	0.003403	protein tyrosine phosphatase, non-receptor type 7
31584_at	down	0.003438	tumor protein, translationally-controlled 1
40610_at	down	0.003441	zinc finger RNA binding protein
108_g_at	up	0.003453	
32590_at	down	0.003459	nucleolin
38516_at	up	0.003465	sodium channel, voltage-gated, type I, beta
33113_at	down	0.003483	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2



34337_s_at	down	0.003512	likely ortholog of mouse metal response element binding transcription factor 2
35976_at	up	0.003514	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1
33622_at	up	0.003533	calcium channel, voltage-dependent, L type, alpha 1C subunit
552_at	up	0.003551	Rho GTPase activating protein 1
36571_at	down	0.00356	topoisomerase (DNA) II beta 180kDa
36887_f_at	up	0.003595	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1
1662_r_at	up	0.003647	Antigen, Prostate Specific, Alt. Splice Form 2
40555_at	down	0.003673	ras homolog gene family, member Q
1389_at	up	0.003688	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
37729_at	down	0.003702	exportin 1 (CRM1 homolog, yeast)
34485_r_at	up	0.003769	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
582_g_at	down	0.003786	nuclear receptor subfamily 2, group C, member 1
38415_at	down	0.003786	protein tyrosine phosphatase type IVA, member 2
2070_i_at	up	0.003801	mitogen-activated protein kinase 8
40392_at	up	0.003801	caudal type homeo box transcription factor 2
35761_at	down	0.003805	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
36793_at	up	0.003865	hypothetical protein AY099107
31859_at	up	0.003871	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)
40928_at	down	0.003876	SOCS box-containing WD protein SWIP-1
41253_s_at	down	0.003901	chorionic somatomammotropin hormone 2
1724_at	up	0.003958	E2F transcription factor 4, p107/p130-binding
37448_s_at	up	0.003965	GNAS complex locus
34081_at	up	0.004003	
40098_at	up	0.004012	EH-domain containing 1
38915_at	up	0.004044	KIAA0563 gene product
37523_at	up	0.004046	acyl-Coenzyme A dehydrogenase, long chain
36179_at	up	0.004048	mitogen-activated protein kinase-activated protein kinase 2
37481_at	down	0.00405	cell division cycle 40 homolog (yeast)
40376_at	up	0.004057	arylsulfatase E (chondrodysplasia punctata 1)
1862_at	up	0.004074	ataxia telangiectasia mutated (includes complementation groups A, C and D)
40497_at	up	0.004088	homologous to yeast nitrogen permease (candidate tumor suppressor)
35317_at	down	0.004109	meningioma expressed antigen 5 (hyaluronidase)
2051_at	up	0.004115	O-6-methylguanine-DNA methyltransferase
1759_f_at	up	0.00415	cytochrome P450, family 3, subfamily A, polypeptide 7
35842_at	down	0.00418	
276_at	down	0.004191	DnaJ (Hsp40) homolog, subfamily A, member 1
38661_at	up	0.004217	RNA-binding region (RNP1, RRM) containing 1

39086_g_at	down	0.004239	single-stranded DNA binding protein
35861_at	up	0.004246	sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase)
38756_at	up	0.004248	RAP1A, member of RAS oncogene family
34441_at	up	0.004253	
AFFX-HSAC07/X00351_5_at	up	0.004262	actin, beta
39169_at	down	0.004272	Sec61 gamma
1128_s_at	up	0.004279	chemokine (C-C motif) receptor 1
38882_r_at	up	0.004292	tripartite motif-containing 16
1929_at	down	0.004324	angiopoietin 1
32088_at	down	0.004339	basic leucine zipper nuclear factor 1 (JEM-1)
38558_at	up	0.004345	myelin associated glycoprotein
31385_at	up	0.004347	ribosomal protein L28
32011_g_at	up	0.004354	hypothetical protein EAN57
494_at	up	0.004374	interleukin 13
38326_at	up	0.004396	putative lymphocyte G0/G1 switch gene
33351_at	down	0.004415	translation factor sui1 homolog
34885_at	up	0.004455	synaptogyrin 2
38443_at	down	0.004483	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)
40643_at	up	0.004486	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B)
37769_at	up	0.004498	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4
34307_at	down	0.004507	transmembrane 9 superfamily member 2
40083_at	down	0.004509	KIAA0625 protein
40649_at	up	0.004524	proprotein convertase subtilisin/kexin type 1
32227_at	down	0.004544	proteoglycan 1, secretory granule
36114_r_at	up	0.004572	troponin T1, skeletal, slow
31549_at	up	0.004598	MAS1 oncogene
39688_at	up	0.004617	requiem, apoptosis response zinc finger gene
1620_at	up	0.004646	cadherin 6, type 2, K-cadherin (fetal kidney)
40601_at	down	0.004663	beta-amyloid binding protein precursor
AFFX-BioDn-5_st	up	0.004695	
39145_at	up	0.004699	myosin, light polypeptide 9, regulatory
1091_at	up	0.004758	protein kinase, cAMP-dependent, regulatory, type I, beta
36029_at	up	0.004763	chromosome 11 open reading frame 8
41237_at	up	0.004771	major histocompatibility complex, class I, A
1104_s_at	up	0.004778	heat shock 70kDa protein 1A

38590_r_at	down	0.004787	prothymosin, alpha (gene sequence 28)
38280_s_at	up	0.004802	neurotrophic tyrosine kinase, receptor, type 2
40943_at	up	0.004812	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)
36557_at	up	0.004814	calcium channel, voltage-dependent, beta 1 subunit
759_at	up	0.004832	prostaglandin I2 (prostacyclin) synthase
201_s_at	up	0.004856	beta-2-microglobulin
36581_at	down	0.004873	glycyl-tRNA synthetase
39825_at	up	0.00488	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1
31471_at	up	0.004912	
37511_at	up	0.004922	B9 protein
33948_at	up	0.004978	corticotropin releasing hormone receptor 2
39594_f_at	up	0.005046	metallothionein 1H
41154_r_at	down	0.005048	catenin (cadherin-associated protein), alpha 1, 102kDa
36173_r_at	down	0.005061	adaptor-related protein complex 3, delta 1 subunit
41812_s_at	down	0.005062	nucleoporin 210
34879_at	down	0.005073	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
33301_g_at	up	0.005075	cell division cycle 2-like 2
32701_at	up	0.005095	armadillo repeat gene deletes in velocardiofacial syndrome
37450_r_at	up	0.005122	GNAS complex locus
600_at	down	0.005135	RAB5A, member RAS oncogene family
1064_at	down	0.005246	PTK9 protein tyrosine kinase 9
38562_g_at	up	0.005247	down-regulated in metastasis
41850_s_at	up	0.005324	hepatitis delta antigen-interacting protein A
35826_at	up	0.005331	suppressor of Ty 5 homolog (S. cerevisiae)
38820_at	down	0.005384	15 kDa selenoprotein
1269_at	down	0.005394	phosphoinositide-3-kinase, regulatory subunit, polypeptic 1 (p85 alpha)
37726_at	down	0.005424	mitochondrial ribosomal protein L3
34155_s_at	up	0.005435	tyrosinase (oculocutaneous albinism IA)
37296_at	down	0.005438	ADP-ribosylation factor-like 1
38060_at	down	0.005484	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
36734_at	up	0.005503	small proline-rich protein 2A
36107_at	down	0.005549	ATP synthase, H+ transporting, mitochondrial F0 complex subunit F6
36961_at	down	0.00558	cervical cancer 1 protooncogene
31386_at	up	0.005585	immunoglobulin kappa variable 1/OR15-118

38939_r_at	up	0.00562	T-box, brain, 1
34824_at	down	0.005649	ubiquitin 2
41443_at	up	0.005702	SEC7 homolog
411_i_at	up	0.005711	interferon induced transmembrane protein 2 (1-8D)
32442_at	up	0.005715	
31481_s_at	down	0.005719	thymosin, beta 10
32726_g_at	down	0.005746	BH3 interacting domain death agonist
34326_at	down	0.005796	coatamer protein complex, subunit beta
126_s_at	up	0.005887	synovial sarcoma, X breakpoint 2
40027_at	down	0.005902	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex subunit s (factor B)
324_f_at	down	0.005902	
41292_at	down	0.005909	heterogeneous nuclear ribonucleoprotein H1 (H)
32394_s_at	down	0.005972	ribosomal protein L23
37560_at	up	0.006036	FLJ00133 protein
38398_at	up	0.006052	MAP-kinase activating death domain
38448_at	up	0.006057	actinin, alpha 2
32859_at	down	0.006069	signal transducer and activator of transcription 1, 91kDa
33535_at	up	0.006079	purinergic receptor P2X, ligand-gated ion channel, 1
35886_at	up	0.006119	protein kinase C and casein kinase substrate in neurons
1930_at	up	0.00618	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
37970_at	up	0.006192	mitogen-activated protein kinase 8 interacting protein 3
41677_at	down	0.006198	interleukin 15 receptor, alpha
38966_at	up	0.006205	glycoprotein, synaptic 2
40137_at	down	0.006261	protein tyrosine phosphatase, non-receptor type 1
32010_at	up	0.006291	hypothetical protein EAN57
34557_at	up	0.006316	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)
39310_at	up	0.006345	bradykinin receptor B2
38412_at	up	0.006424	protein phosphatase 1, regulatory (inhibitor) subunit 11
35266_at	down	0.006494	bladder cancer associated protein
37693_at	down	0.006535	numb homolog (Drosophila)
32802_at	down	0.00654	similar to S. cerevisiae SSM4
39099_at	down	0.00654	Sec23 homolog A (S. cerevisiae)
41376_i_at	up	0.006549	UDP glycosyltransferase 2 family, polypeptide B7
38209_at	up	0.006601	prostaglandin E receptor 1 (subtype EP1), 42kDa
37337_at	down	0.006676	small nuclear ribonucleoprotein polypeptide G
2036_s_at	down	0.006697	CD44 antigen (homing function and Indian blood group system)
39168_at	up	0.00673	Ac-like transposable element
36229_at	up	0.006732	interleukin 17 receptor
39034_at	down	0.006748	DKFZP564O123 protein

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39428_at	down	0.00676	lymphocyte adaptor protein
33181_at	down	0.006774	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
40225_at	up	0.006775	cyclin G associated kinase
37939_at	up	0.006831	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C
35814_at	down	0.006855	dendritic cell protein
40790_at	down	0.006931	basic helix-loop-helix domain containing, class B, 2
36779_at	up	0.006977	fatty acid binding protein 6, ileal (gastrotropin)
1525_s_at	up	0.006997	fibroblast growth factor 8 (androgen-induced)
34630_s_at	up	0.007011	dynein, axonemal, heavy polypeptide 9
40306_at	up	0.007012	v-raf murine sarcoma viral oncogene homolog B1
37731_at	down	0.007018	epidermal growth factor receptor pathway substrate 15
35512_at	up	0.007135	
39926_at	down	0.007144	MAD, mothers against decapentaplegic homolog 5 (Drosophila)
34397_at	down	0.007213	acid-inducible phosphoprotein
39784_at	down	0.007234	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
39454_f_at	up	0.007249	T-cell leukemia, homeobox 2
35892_at	up	0.00729	complement component (3b/4b) receptor 1, including Knops blood group system
38848_at	up	0.007302	zymogen granule protein 16
2094_s_at	up	0.007347	v-fos FBJ murine osteosarcoma viral oncogene homolog
34559_at	up	0.007367	
35643_at	down	0.007384	nucleobindin 2
40885_s_at	down	0.007411	syntaxin 16
40847_at	up	0.007437	flavoprotein oxidoreductase MICAL2
237_s_at	down	0.007442	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
35286_r_at	down	0.007473	putative nucleic acid binding protein RY-1
518_at	up	0.007484	nuclear receptor subfamily 1, group H, member 2
162_at	up	0.007506	ubiquitin specific protease 11
38226_at	down	0.007549	hypothetical protein FLJ10569
32134_at	down	0.007574	testis derived transcript (3 LIM domains)
33385_g_at	down	0.0076	calpastatin
35716_at	up	0.007601	sulfotransferase family, cytosolic, 1C, member 1
38447_at	up	0.007604	adrenergic, beta, receptor kinase 1
38992_at	down	0.007658	DEK oncogene (DNA binding)
33889_s_at	up	0.007667	DiGeorge syndrome critical region gene 2
38162_at	up	0.007683	regulating synaptic membrane exocytosis 2
38707_r_at	up	0.007701	E2F transcription factor 4, p107/p130-binding

41212_r_at	down	0.007709	Williams-Beuren syndrome chromosome region 1
32740_at	down	0.007724	KIAA0941 protein
35246_at	up	0.007732	TYRO3 protein tyrosine kinase
32090_at	up	0.007747	nicotinamide nucleotide adenylyltransferase 2
35411_at	up	0.007824	chromosome 16 open reading frame 7
31957_r_at	up	0.007826	ribosomal protein, large, P1
38084_at	down	0.007858	chromobox homolog 3 (HP1 gamma homolog, Drosophil
39136_at	down	0.007923	oxidative-stress responsive 1
33727_r_at	up	0.007975	tumor necrosis factor receptor superfamily, member 6b, decoy
39160_at	down	0.007995	pyruvate dehydrogenase (lipoamide) beta
584_s_at	down	0.008042	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)
36317_at	up	0.008056	coronin, actin binding protein, 2A
32298_at	up	0.008057	a disintegrin and metalloproteinase domain 2 (fertilin bet
39714_at	down	0.008105	SH3 domain binding glutamic acid-rich protein like
36523_at	down	0.00813	ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)
37411_at	up	0.008164	centaurin, beta 1
33247_at	down	0.008182	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
32836_at	up	0.008183	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)
36473_at	up	0.008198	ubiquitin specific protease 20
1499_at	down	0.0082	farnesyltransferase, CAAX box, alpha
33633_at	up	0.008238	purinergic receptor P2Y, G-protein coupled, 11
38736_at	down	0.008238	WD repeat domain 1
31796_at	up	0.008255	kinesin family member 1C
36608_at	down	0.008257	malate dehydrogenase 1, NAD (soluble)
32725_at	down	0.008258	BH3 interacting domain death agonist
34615_at	up	0.008286	keratin 12 (Meesmann corneal dystrophy)
39517_at	down	0.008321	HTGN29 protein
34503_at	up	0.008323	
37740_r_at	down	0.008356	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
39442_at	down	0.008385	unc-50 related
38395_at	down	0.00841	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
33336_at	up	0.008411	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)
35738_at	down	0.008416	high mobility group nucleosomal binding domain 4
39473_r_at	up	0.008426	protein tyrosine phosphatase type IVA, member 3
32070_at	up	0.008449	protein tyrosine phosphatase, receptor type, C-associated protein
36824_at	up	0.008494	astrotactin

35492_at	up	0.00852	cytochrome P450, family 4, subfamily F, polypeptide 12
40146_at	down	0.008529	RAP1B, member of RAS oncogene family
36660_at	down	0.00856	RAB11A, member RAS oncogene family
33791_at	up	0.008585	deleted in lymphocytic leukemia, 1
37475_at	up	0.008624	DKFZP434J046 protein
34480_at	up	0.008635	cadherin 16, KSP-cadherin
35278_at	up	0.008637	ribosomal protein S29
37720_at	down	0.008641	heat shock 60kDa protein 1 (chaperonin)
35612_at	up	0.00866	DKFZP564P1916 protein
36090_at	down	0.0087	transducin (beta)-like 2
41722_at	down	0.008706	nicotinamide nucleotide transhydrogenase
1228_s_at	down	0.008746	meningioma expressed antigen 6 (coiled-coil proline-rich)
34323_at	down	0.008748	thyroid receptor interacting protein 15
36975_at	down	0.00878	hypothetical protein MGC8721
875_g_at	up	0.008864	chemokine (C-C motif) ligand 2
1908_at	up	0.008924	ets variant gene 3
33665_s_at	down	0.00895	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)
37351_at	up	0.008972	uridine phosphorylase
38656_s_at	down	0.008989	hypothetical protein MGC5576
33845_at	down	0.00901	heterogeneous nuclear ribonucleoprotein H1 (H)
1187_at	up	0.009027	ligase III, DNA, ATP-dependent
31700_at	up	0.009079	G protein-coupled receptor 35
37166_at	up	0.009158	3-hydroxyanthranilate 3,4-dioxygenase
35521_at	up	0.009159	claudin 9
39384_at	up	0.009225	ELAV (embryonic lethal, abnormal vision, Drosophila)-lik 1 (Hu antigen R)
31495_at	up	0.009226	chemokine (C motif) ligand 2
1011_s_at	down	0.009274	tyrosine 3-monooxygenase/tryptophan 5-monooxygenas activation protein, epsilon polypeptide
33150_at	down	0.009294	disrupter of silencing 10
41118_at	up	0.009318	hypothetical protein FLJ13639
34370_at	down	0.009349	archain 1
AFFX- HUMISGF3A/M9 7935_3_at	down	0.009365	signal transducer and activator of transcription 1, 91kDa
32778_at	down	0.009367	inositol 1,4,5-triphosphate receptor, type 1
41223_at	down	0.009391	cytochrome c oxidase subunit Va
32452_at	up	0.009405	cyclin-dependent kinase 3
39326_at	up	0.009436	ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a isoform 1
36264_at	up	0.00945	megakaryocyte-associated tyrosine kinase
35136_at	down	0.009509	nuclear transport factor 2-like export factor 2
34448_s_at	up	0.009565	caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2)
36012_at	down	0.00959	progesterone-induced blocking factor 1

39375_g_at	up	0.009636	G-2 and S-phase expressed 1
39023_at	down	0.009731	isocitrate dehydrogenase 1 (NADP+), soluble
41771_g_at	up	0.009755	monoamine oxidase A
37579_at	up	0.009808	cytoplasmic FMR1 interacting protein 2
36931_at	up	0.009886	transgelin
37328_at	down	0.009996	pleckstrin
38058_at	up	0.010002	dermatopontin
40802_at	down	0.010028	DKFZP434C212 protein
1675_at	down	0.010041	RAS p21 protein activator (GTPase activating protein) 1
35741_at	down	0.01005	phosphatidylinositol-4-phosphate 5-kinase, type II, beta
38046_at	down	0.01007	IK cytokine, down-regulator of HLA II
39686_g_at	down	0.010084	like mouse brain protein E46
850_r_at	up	0.010147	insulin receptor substrate 1
36152_at	up	0.010166	GDP dissociation inhibitor 1
40931_at	down	0.010287	CGI-100 protein
38375_at	down	0.010289	esterase D/formylglutathione hydrolase
31726_at	up	0.010328	gamma-aminobutyric acid (GABA) A receptor, alpha 3
33902_at	up	0.01033	glycerol-3-phosphate dehydrogenase 1 (soluble)
32749_s_at	up	0.010344	filamin A, alpha (actin binding protein 280)
33331_at	up	0.010358	BENE protein
35276_at	up	0.010366	claudin 4
34196_at	down	0.010443	ocular development-associated gene
1211_s_at	down	0.010444	CASP2 and RIPK1 domain containing adaptor with death domain
133_at	down	0.010451	cathepsin C
41342_at	down	0.010536	RAN binding protein 1
39605_at	up	0.010552	forkhead box G1B
35412_at	up	0.010552	cytochrome P450, family 4, subfamily A, polypeptide 11
33645_at	up	0.01057	GM2 ganglioside activator protein
34778_at	up	0.010585	
39281_at	up	0.010599	Rho guanine nucleotide exchange factor (GEF) 11
38676_at	down	0.010653	stress 70 protein chaperone, microsome-associated, 60kDa
37254_at	up	0.010656	zinc finger protein 133 (clone pHZ-13)
38631_at	down	0.010686	tumor necrosis factor, alpha-induced protein 2
33373_at	down	0.010724	
32816_at	down	0.01074	small glutamine-rich tetratricopeptide repeat (TPR)-containing
567_s_at	up	0.01077	promyelocytic leukemia
34707_at	up	0.010772	chromodomain helicase DNA binding protein 3
34785_at	down	0.010772	KIAA1025 protein
AFFX-BioDn-3_at	up	0.0108	



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34894_r_at	up	0.010828	protease, serine, 22
1787_at	down	0.010871	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
35960_at	up	0.010922	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
33679_f_at	up	0.010949	tubulin, beta, 2
33458_r_at	down	0.010981	histone 1, H2bc
32212_at	down	0.011004	programmed cell death 8 (apoptosis-inducing factor)
32210_at	up	0.011012	phosphoglucomutase 1
38976_at	up	0.011013	coronin, actin binding protein, 1A
41657_at	up	0.011105	serine/threonine kinase 11 (Peutz-Jeghers syndrome)
39760_at	down	0.011179	quaking homolog, KH domain RNA binding (mouse)
39592_r_at	down	0.011186	fibrinogen-like 2
38269_at	up	0.011209	protein kinase D2
39212_at	up	0.011221	hypothetical protein FLJ11191
41081_at	up	0.0113	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)
36272_r_at	up	0.011309	peripheral myelin protein 2
36669_at	up	0.011328	FBJ murine osteosarcoma viral oncogene homolog B
40874_at	down	0.011345	endothelial differentiation-related factor 1
1877_g_at	down	0.011363	
36886_f_at	up	0.011466	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3
36924_r_at	up	0.011516	secretogranin II (chromogranin C)
38439_at	up	0.011558	nuclear factor (erythroid-derived 2)-like 1
39733_at	down	0.011569	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
33034_at	up	0.011597	rhomboid, veinlet-like 1 (Drosophila)
32380_at	up	0.01161	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)
41819_at	down	0.011617	FYN binding protein (FYB-120/130)
781_at	down	0.011656	Rab geranylgeranyltransferase, beta subunit
37943_at	down	0.011657	zinc finger, FYVE domain containing 26
41641_at	up	0.011665	GPI-anchored metastasis-associated protein homolog
273_g_at	up	0.011718	gastrin-releasing peptide
36891_at	up	0.01173	putative acyltransferase
32235_at	up	0.011759	mahogunin, ring finger 1
33750_at	up	0.01177	protein tyrosine phosphatase, receptor type, U
2063_at	down	0.011827	excision repair cross-complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum, complementation group G (Cockayne syndrome))
466_at	down	0.011856	general transcription factor II, i
38755_at	up	0.011889	Fas (TNFRSF6)-associated via death domain

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37850_at	up	0.011942	hypothetical protein dJ462O23.2
36894_at	up	0.011976	plakophilin 4
38710_at	up	0.012032	ubiquitin-specific protease otubain 1
35165_at	down	0.012038	hypothetical protein MGC13033
37728_r_at	down	0.012091	reticulocalbin 2, EF-hand calcium binding domain
32837_at	up	0.0121	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
1717_s_at	down	0.012108	baculoviral IAP repeat-containing 3
933_f_at	down	0.012134	zinc finger protein 91 (HPF7, HTF10)
37919_at	up	0.012214	solute carrier family 21 (prostaglandin transporter), member 2
1196_at	up	0.012219	chromosome condensation 1
1285_at	up	0.012233	
41490_at	down	0.012323	phosphoribosyl pyrophosphate synthetase 2
504_at	down	0.012336	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
34146_at	up	0.01236	8-oxoguanine DNA glycosylase
36336_s_at	up	0.012444	KIAA0963 protein
36198_at	down	0.012492	translocase of outer mitochondrial membrane 20 (yeast) homolog
32000_g_at	up	0.012498	ATP-binding cassette, sub-family A (ABC1), member 1
41257_at	down	0.012502	calpastatin
34768_at	down	0.012514	thioredoxin domain containing
31977_at	up	0.012525	guanylate cyclase 2D, membrane (retina-specific)
39628_at	up	0.012571	RAB9A, member RAS oncogene family
36583_at	down	0.012698	sorting nexin 1
41179_at	down	0.012738	ring finger protein 44
36436_at	up	0.012745	leukocyte cell-derived chemotaxin 2
39327_at	up	0.012808	Melanoma associated gene
31525_s_at	up	0.012813	hemoglobin, alpha 2
1815_g_at	down	0.012835	transforming growth factor, beta receptor II (70/80kDa)
40745_at	up	0.012844	adaptor-related protein complex 1, beta 1 subunit
1795_g_at	up	0.012848	cyclin D3
1079_g_at	up	0.012852	prolactin receptor
40837_at	up	0.012862	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
34440_at	up	0.012898	DiGeorge syndrome critical region gene 9
33433_at	down	0.012905	DKFZP564F0522 protein
40613_at	down	0.012921	chromosome 6 open reading frame 62
40182_s_at	up	0.012959	coactivator-associated arginine methyltransferase-1
36425_at	up	0.012979	nebulette
31995_g_at	up	0.012992	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)

36338_at	up	0.013004	leucine zipper protein 1
34753_at	down	0.013079	synaptobrevin-like 1
41036_at	up	0.01309	hypothetical protein FLJ12242
33568_at	up	0.013116	cholinergic receptor, nicotinic, beta polypeptide 4
36550_at	down	0.013154	Ras and Rab interactor 2
35564_at	up	0.013202	
34334_at	up	0.013236	ephrin-B2
35848_at	down	0.013256	retinoic acid induced 17
33264_at	up	0.013299	rTS beta protein
41080_at	up	0.013323	H2A histone family, member B
40130_at	up	0.013335	folliculin-like 1
32233_at	down	0.013347	torsin family 1, member B (torsin B)
35209_at	down	0.013359	EPM2A (laforin) interacting protein 1
40644_g_at	up	0.013371	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B)
41063_g_at	up	0.013386	likely ortholog of mouse nervous system polycomb 1
37747_at	down	0.013389	annexin A5
31599_f_at	up	0.013395	melanoma antigen, family A, 6
39140_at	down	0.013426	nucleic acid helicase DDXx
41634_at	down	0.013478	KIAA0256 gene product
1789_at	down	0.013483	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)
34385_at	down	0.013542	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa
39955_at	up	0.013562	deleted in lymphocytic leukemia, 2
1147_at	up	0.013573	
40539_at	up	0.013587	myosin IXB
36472_at	down	0.013625	N-myc (and STAT) interactor
40783_s_at	up	0.013679	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide
36171_at	down	0.013705	activated RNA polymerase II transcription cofactor 4
35868_at	up	0.013726	advanced glycosylation end product-specific receptor
1245_i_at	down	0.013758	p21 (CDKN1A)-activated kinase 2
37793_r_at	up	0.013825	RAD51-like 3 (S. cerevisiae)
35082_at	up	0.013847	Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila)
34762_at	up	0.013858	ring finger protein (C3HC4 type) 8
41187_at	down	0.013902	myosin regulatory light chain MRLC2
33879_at	up	0.013908	type I sigma receptor
1652_at	up	0.013938	pim-2 oncogene
40417_at	down	0.013938	chaperonin containing TCP1, subunit 5 (epsilon)
41129_at	down	0.013943	KIAA0033 protein
38420_at	up	0.013954	collagen, type V, alpha 2
34210_at	down	0.014015	CDW52 antigen (CAMPATH-1 antigen)
39344_at	down	0.014023	transformer-2 alpha (htra-2 alpha)
1706_at	up	0.014079	v-raf murine sarcoma 3611 viral oncogene homolog 1
34661_at	up	0.014103	KIAA0350 protein

38993_r_at	down	0.014129	
32184_at	down	0.014139	LIM domain only 2 (rhombotin-like 1)
36631_at	down	0.014147	peroxiredoxin 3
35371_at	up	0.014173	LPS-responsive vesicle trafficking, beach and anchor containing
39640_at	up	0.014174	glutamine-fructose-6-phosphate transaminase 2
36019_at	up	0.014196	serine/threonine kinase 19
37584_at	up	0.014203	Fanconi anemia, complementation group G
36011_at	up	0.014257	syntaxin 10
36482_s_at	up	0.014257	ATPase, Ca++ transporting, ubiquitous
31950_at	down	0.014258	poly(A) binding protein, cytoplasmic 1
37220_at	down	0.014462	Fc fragment of IgG, high affinity Ia, receptor for (CD64)
37121_at	up	0.014557	natural killer cell group 7 sequence
36538_at	up	0.014685	protein phosphatase 1, regulatory (inhibitor) subunit 13B
38686_at	up	0.014734	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit c isoform 1
32695_at	down	0.014748	HIV TAT specific factor 1
32121_at	down	0.014803	phosphoinositide-3-kinase, catalytic, delta polypeptide
37374_at	down	0.014809	annexin A4
41273_at	up	0.014835	FK506 binding protein 12-rapamycin associated protein
32464_at	up	0.014865	defensin, beta 4
34293_at	up	0.014917	kinesin family member C3
37035_at	down	0.014931	stress-associated endoplasmic reticulum protein 1
1318_at	down	0.014941	retinoblastoma binding protein 4
35215_at	down	0.014941	HDCMA18P protein
38572_at	up	0.01496	FGFR1 oncogene partner
32258_r_at	down	0.014963	telomeric repeat binding factor (NIMA-interacting) 1
34646_at	down	0.014971	ribosomal protein S7
33821_at	down	0.014993	homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2
37038_at	down	0.015036	ATP-binding cassette, sub-family D (ALD), member 3
38463_s_at	down	0.015059	adenosine monophosphate deaminase (isoform E)
31668_f_at	up	0.015097	erythrocyte membrane protein band 4.1-like 2
34310_at	up	0.015109	adenine phosphoribosyltransferase
1324_at	up	0.015162	RAD9 homolog (S. pombe)
40989_at	up	0.01517	tetraspan 5
32493_at	up	0.015183	thyrotrophic embryonic factor
39694_at	up	0.015198	hypothetical protein MGC5508
34763_at	down	0.015201	chondroitin sulfate proteoglycan 6 (bamacan)
41134_at	up	0.015209	disks large-associated protein 4
36136_at	up	0.015225	tumor protein p53 inducible protein 11
35973_at	down	0.015225	huntingtin interacting protein 14

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36004_at	up	0.015262	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma
37506_at	down	0.01527	formin binding protein 3
36795_at	up	0.015294	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
31808_at	down	0.015332	inhibitor of growth family, member 3
38829_r_at	down	0.015403	KH-type splicing regulatory protein (FUSE binding protein 2)
34301_r_at	up	0.015458	keratin 17
39392_at	down	0.01557	glyceronephosphate O-acyltransferase
41132_r_at	down	0.015577	heterogeneous nuclear ribonucleoprotein H2 (H')
35952_at	up	0.015587	
31882_at	up	0.015605	RNA, U3 small nucleolar interacting protein 2
40132_g_at	down	0.015651	folistatin-like 1
31999_at	up	0.01568	ATP-binding cassette, sub-family A (ABC1), member 1
32214_at	down	0.015754	thioredoxin-like, 32kDa
38244_at	up	0.015774	hypothetical protein FLJ10178
38841_at	down	0.01586	putative glialblastoma cell differentiation-related
40615_at	down	0.015863	hypothetical protein FLJ21439
36932_at	down	0.015868	general transcription factor IIIC, polypeptide 2, beta 110kDa
40684_at	up	0.015914	GTP cyclohydrolase I feedback regulatory protein
537_f_at	up	0.015947	breakpoint cluster region
40246_at	down	0.015992	discs, large (Drosophila) homolog 1
31924_at	up	0.016021	testicular soluble adenylyl cyclase
952_at	down	0.016057	
33925_at	up	0.016064	neurogranin (protein kinase C substrate, RC3)
41784_at	down	0.016071	SR rich protein
32696_at	down	0.016102	pre-B-cell leukemia transcription factor 3
39857_at	down	0.016137	syntaxin 11
33186_i_at	up	0.01614	
33297_at	down	0.016149	chromosome 6 open reading frame 130
872_i_at	up	0.016203	insulin receptor substrate 1
35080_at	up	0.016227	neurotensin receptor 1 (high affinity)
40933_f_at	up	0.016236	zinc finger, DHHC domain containing 18
38380_at	down	0.016279	POP4 (processing of precursor, S. cerevisiae) homolog
34962_at	up	0.01628	
40203_at	down	0.016313	putative translation initiation factor
31511_at	up	0.016334	ribosomal protein S9
821_s_at	down	0.016432	folate receptor 1 (adult)
37973_at	down	0.016448	sorting nexin 13
229_at	down	0.01645	CCAAT-box-binding transcription factor
1159_at	up	0.016461	interleukin 7
343_s_at	up	0.016526	ectonucleotide pyrophosphatase/phosphodiesterase 1

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40315_at	up	0.016527	serine protease inhibitor, Kazal type, 5
34813_at	down	0.016531	eukaryotic translation initiation factor 1A
38868_at	up	0.01656	Fc fragment of IgA, receptor for
1601_s_at	down	0.016625	insulin-like growth factor binding protein 5
40189_at	down	0.016702	SET translocation (myeloid leukemia-associated)
34679_at	up	0.016704	breakpoint cluster region
35915_at	up	0.01671	inhibin, beta C
40619_at	up	0.016734	ubiquitin carrier protein
39740_g_at	down	0.016741	nascent-polypeptide-associated complex alpha polypeptide
38016_at	down	0.016744	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
1707_g_at	up	0.01675	v-ras murine sarcoma 3611 viral oncogene homolog 1
41459_at	down	0.016767	tripeptidyl peptidase II
41524_at	down	0.01681	inositol polyphosphate-1-phosphatase
41085_at	up	0.016818	polymerase (DNA directed), epsilon 2 (p59 subunit)
155_s_at	down	0.016819	ubiquitin-like 1 (sentrin)
1650_g_at	up	0.016871	chromosome 20 open reading frame 16
41059_at	down	0.016883	leukocyte membrane antigen
32700_at	down	0.016939	guanylate binding protein 2, interferon-inducible
41749_at	down	0.01696	chromosome 21 open reading frame 33
33603_at	up	0.016974	ATP-binding cassette, sub-family D (ALD), member 1
36159_s_at	down	0.017029	prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
37843_i_at	up	0.017095	class I cytokine receptor
1555_f_at	up	0.017101	cytochrome P450, family 2, subfamily A, polypeptide 7
36445_at	up	0.017109	chemokine (C-C motif) ligand 23
37449_i_at	up	0.017262	GNAS complex locus
31613_at	up	0.017304	laminin, beta 4
31746_at	up	0.017309	zinc finger protein 204
37962_r_at	down	0.017344	syntaxin binding protein 3
2044_s_at	down	0.017376	retinoblastoma 1 (including osteosarcoma)
35327_at	down	0.017394	eukaryotic translation initiation factor 3, subunit 3 gamma 40kDa
34730_g_at	up	0.017407	trophinin
31406_at	up	0.017412	G protein-coupled receptor 50
31932_f_at	down	0.017423	basic transcription factor 3
442_at	down	0.017431	tumor rejection antigen (gp96) 1
151_s_at	up	0.017469	hypothetical protein DKFZp434N0650
40817_at	up	0.017498	nucleobindin 1

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34637_f_at	up	0.017511	alcohol dehydrogenase 1A (class I), alpha polypeptide
32350_at	down	0.017517	mucosa associated lymphoid tissue lymphoma translocation gene 1
33778_at	up	0.017561	chromosome 22 open reading frame 4
31687_f_at	up	0.017608	hemoglobin, beta
AFFX-BioC-3_at	up	0.017611	
1420_s_at	down	0.017633	eukaryotic translation initiation factor 4A, isoform 2
33441_at	up	0.017697	T-cell leukemia translocation altered gene
37871_at	up	0.017737	islet amyloid polypeptide
32971_at	up	0.017788	Friedreich ataxia region gene X123
39547_at	up	0.017849	RAN binding protein 9
37727_i_at	down	0.017866	reticulocalbin 2, EF-hand calcium binding domain
33467_at	up	0.017871	CMRF35 leukocyte immunoglobulin-like receptor
32287_s_at	up	0.017884	killer cell lectin-like receptor subfamily C, member 3
1903_at	down	0.017927	
36195_at	down	0.018011	isocitrate dehydrogenase 3 (NAD+) alpha
40609_at	up	0.018045	helicase with SNF2 domain 1
32599_at	down	0.018087	tuberous sclerosis 1
37015_at	down	0.018105	aldehyde dehydrogenase 1 family, member A1
36590_at	up	0.018149	solute carrier family 16 (monocarboxylic acid transporters), member 2 (putative transporter)
38830_at	up	0.018172	hypothetical protein FLJ11198
1986_at	down	0.018179	retinoblastoma-like 2 (p130)
192_at	down	0.018213	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa
35630_at	up	0.018226	lethal giant larvae homolog 2 (Drosophila)
40637_at	down	0.018269	heat shock 70kDa protein 8
31768_at	up	0.018276	histone 1, H2ai
34253_at	down	0.018328	nucleoporin 160kDa
36783_f_at	down	0.018333	Krueppel-related zinc finger protein
31914_at	up	0.018338	chromodomain helicase DNA binding protein 1-like
41374_at	up	0.0184	ribosomal protein S6 kinase, 70kDa, polypeptide 2
40754_at	up	0.018431	general transcription factor IIH, polypeptide 3, 34kDa
34857_at	down	0.018445	hypothetical protein FLJ20986
33534_at	up	0.018485	endothelial cell-specific molecule 1
41852_at	up	0.018525	rearranged L-myc fusion sequence
32181_at	up	0.018613	flotillin 2
37967_at	up	0.01865	leukocyte specific transcript 1
33084_at	up	0.018756	complexin 2
32345_at	up	0.018764	
1295_at	down	0.018786	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)
40166_at	down	0.01879	likely ortholog of mouse WD-40-repeat-containing protein with a SOCS box 2

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38068_at	down	0.018828	autocrine motility factor receptor
1038_s_at	down	0.018932	interferon gamma receptor 1
41601_at	down	0.018953	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)
2057_g_at	up	0.018958	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
226_at	down	0.018995	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
32850_at	down	0.018999	nucleoporin 153kDa
36186_at	up	0.01902	RNA binding protein S1, serine-rich domain
34644_at	up	0.019096	beta-2-microglobulin
300_f_at	down	0.019103	
825_at	down	0.019195	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
35938_at	down	0.019217	phospholipase A2, group IVA (cytosolic, calcium-dependent)
36539_at	up	0.019221	immunoglobulin lambda locus
34086_at	up	0.019292	endothelial differentiation, sphingolipid G-protein-coupled receptor, 5
34525_at	up	0.019298	T-cell leukemia/lymphoma 1B
38007_at	up	0.019318	neurofibromin 2 (bilateral acoustic neuroma)
36463_at	down	0.019332	BCL2-associated athanogene 5
33109_f_at	up	0.019346	SRY (sex determining region Y)-box 2
40309_at	up	0.019388	carbonic anhydrase IX
34349_at	down	0.019479	SEC63-like (S. cerevisiae)
691_g_at	up	0.019503	procollagen-proline, 2-oxoglutarate 4-dioxygenase (prolir 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)
38657_s_at	up	0.019523	clathrin, light polypeptide (Lca)
40365_at	up	0.019556	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
36576_at	down	0.019565	H2A histone family, member Y
2004_at	down	0.019576	mitogen-activated protein kinase kinase 1
31890_s_at	down	0.019638	zinc finger protein 143 (clone pHZ-1)
510_g_at	down	0.019641	MAD, mothers against decapentaplegic homolog 4 (Drosophila)
32183_at	down	0.01973	splicing factor, arginine/serine-rich 11
37812_at	up	0.019731	cut-like 2 (Drosophila)
41131_f_at	down	0.019743	heterogeneous nuclear ribonucleoprotein H2 (H')
32265_at	up	0.019747	nuclear receptor subfamily 4, group A, member 1
33771_at	up	0.019763	T-cell activation leucine repeat-rich protein
531_at	down	0.019841	GLI pathogenesis-related 1 (glioma)
34796_at	down	0.01992	translocation associated membrane protein 1
35312_at	up	0.019979	MCM2 minichromosome maintenance deficient 2, mitotir (S. cerevisiae)
35303_at	down	0.020035	insulin induced gene 1



36547_r_at	up	0.020045	KIAA0542 gene product
35650_at	down	0.020047	KIAA0356 gene product
34387_at	down	0.020082	KIAA0205 gene product
40208_at	up	0.020123	growth differentiation factor 11
41147_at	down	0.020124	hypothetical protein MGC4276 similar to CG8198
32171_at	down	0.020139	eukaryotic translation initiation factor 5
35798_at	up	0.020169	NS1-associated protein 1
39657_at	up	0.02024	keratin 4
34147_g_at	up	0.02024	8-oxoguanine DNA glycosylase
41195_at	down	0.020265	LIM domain containing preferred translocation partner in lipoma
36514_at	down	0.02029	cell growth regulatory with ring finger domain
39833_at	up	0.020298	misshapen/NIK-related kinase
38717_at	down	0.02043	DKFZP586A0522 protein
34884_at	up	0.020442	carbamoyl-phosphate synthetase 1, mitochondrial
35674_at	down	0.020444	peptidyl arginine deiminase, type II
930_at	up	0.020469	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha
40141_at	down	0.020498	cullin 4B
35012_at	down	0.020538	myeloid cell nuclear differentiation antigen
31326_at	up	0.020632	
38088_r_at	up	0.020721	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)
41335_at	down	0.020743	DKFZP566O1646 protein
35048_at	up	0.020747	glutamate receptor, ionotropic, AMPA 3
37545_at	up	0.020815	secretory carrier membrane protein 5
39750_at	up	0.020847	zinc finger, DHHC domain containing 3
37811_at	up	0.020897	calcium channel, voltage-dependent, alpha 2/delta subunit 2
31728_at	up	0.02093	major histocompatibility complex, class II, DO alpha
39178_at	down	0.020932	reticulon 1
40636_at	up	0.020943	flotillin 1
1062_g_at	down	0.02097	interleukin 10 receptor, alpha
39400_at	up	0.020978	KIAA1055 protein
34383_at	down	0.021052	ubiquitin specific protease 1
39793_at	down	0.021068	glioblastoma amplified sequence
36934_at	down	0.021189	chromosome 20 open reading frame 111
38815_at	down	0.021221	actin related protein 2/3 complex, subunit 1A, 41kDa
38780_at	down	0.021235	aldo-keto reductase family 1, member A1 (aldehyde reductase)
38685_at	down	0.021249	syntaxin 12
34751_at	down	0.021264	zinc finger and BTB domain containing 1
39108_at	up	0.021289	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
33908_at	up	0.02134	calpain 1, (mu/I) large subunit
32895_f_at	up	0.021352	HIV-1 Rev binding protein-like
37409_at	down	0.021533	SFRS protein kinase 2
32575_at	up	0.021556	nucleosome assembly protein 1-like 4

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36952_at	up	0.021656	mucosa associated lymphoid tissue lymphoma translocation gene 1
34767_at	down	0.021706	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
AFFX-HUMGAPDH/M3	up	0.021712	modulator of apoptosis 1
3197_M_st			glyceraldehyde-3-phosphate dehydrogenase
352_at	up	0.021712	phosphatidylinositol transfer protein
38383_at	down	0.021745	5-methyltetrahydrofolate-homocysteine methyltransferase
36648_at	down	0.021783	cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa
40431_at	down	0.021788	KIAA0431 protein
36433_at	up	0.021793	glycine receptor, alpha 3
35918_at	up	0.021822	deleted in lung and esophageal cancer 1
37078_at	up	0.021832	CD3Z antigen, zeta polypeptide (TiT3 complex)
33278_at	up	0.021853	SA hypertension-associated homolog (rat)
39839_at	down	0.021855	cold shock domain protein A
39088_at	up	0.021896	seven transmembrane domain protein
35036_at	down	0.02195	complement component 1, q subcomponent, receptor 1
33382_at	down	0.021991	N-acylsphingosine amidohydrolase (acid ceramidase)-like
41520_at	up	0.022029	hypothetical protein LOC284352
32563_at	down	0.022071	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 3 polypeptide
40457_at	down	0.022156	splicing factor, arginine/serine-rich 3
36404_at	up	0.022162	glucagon-like peptide 1 receptor
893_at	up	0.022233	ubiquitin carrier protein
37691_at	up	0.0223	MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)
36191_at	down	0.022333	transcription factor A, mitochondrial
40801_at	down	0.022358	DKFZP434C212 protein
32953_at	up	0.022369	CD5 antigen (p56-62)
35450_s_at	up	0.022389	general transcription factor II, i
41726_at	up	0.022435	endothelin converting enzyme 1
37463_r_at	up	0.022459	splicing factor 3a, subunit 2, 66kDa
37622_r_at	down	0.022516	PC4 and SFRS1 interacting protein 2
263_g_at	down	0.022574	adenosylmethionine decarboxylase 1
34400_at	down	0.022648	low molecular mass ubiquinone-binding protein (9.5kD)
39501_f_at	up	0.022704	amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein
2032_s_at	up	0.022708	Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
31879_at	down	0.022724	far upstream element (FUSE) binding protein 3

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2001_at	down	0.022731	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
41185_f_at	down	0.022767	SMT3 suppressor of mif two 3 homolog 2 (yeast)
41829_at	up	0.022808	likely ortholog of mouse Ia related protein
41388_at	up	0.022831	Meis1, myeloid ecotropic viral integration site 1 homolog (mouse)
38401_s_at	up	0.022852	DKFZP434D1335 protein
452_at	down	0.022861	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
1649_at	up	0.022875	chromosome 20 open reading frame 16
38106_at	down	0.022878	TGF beta-inducible nuclear protein 1
34704_r_at	up	0.022898	chorionic somatomammotropin hormone 2
1388_g_at	down	0.022922	vitamin D (1,25- dihydroxyvitamin D3) receptor
35432_at	down	0.022924	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)
AFFX-HSAC07/X00351_3_at	up	0.022931	actin, beta
37493_at	down	0.023078	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
32646_at	up	0.023083	KIAA0449 protein
32001_s_at	up	0.023099	paired basic amino acid cleaving system 4
886_at	down	0.023115	deoxycytidine kinase
32858_at	up	0.023123	ubiquitin 1
707_s_at	up	0.023162	
38791_at	up	0.02319	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
40579_at	down	0.023229	HIV-1 Rev binding protein
41214_at	down	0.023253	ribosomal protein S4, Y-linked
37393_at	down	0.02326	hairy and enhancer of split 1, (Drosophila)
35487_at	up	0.023272	bromodomain, testis-specific
32866_at	up	0.023293	KIAA0605 gene product
34773_at	down	0.023349	tubulin-specific chaperone a
32669_at	down	0.023384	suppressor of cytokine signaling 5
37697_s_at	down	0.023475	voltage-dependent anion channel 2
39809_at	down	0.023498	HMG-box containing protein 1
33268_at	up	0.023524	Smcx homolog, X chromosome (mouse)
33320_at	down	0.023552	MHC class I region ORF
32297_s_at	up	0.023584	killer cell lectin-like receptor subfamily C, member 2
34059_at	up	0.023596	Pvt1 oncogene homolog, MYC activator (mouse)
38732_at	down	0.023596	chloride channel, nucleotide-sensitive, 1A
41716_at	down	0.023639	rabconnectin-3
172_at	up	0.023662	inositol polyphosphate-5-phosphatase, 145kDa

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40361_at	up	0.023669
38693_at	down	0.02374
40108_at	down	0.02382
34306_at	down	0.023824
34967_at	up	0.02384
40363_r_at	up	0.023842
32264_at	up	0.023943
34084_at	up	0.023985
39742_at	down	0.024012
33298_at	down	0.024013
37819_at	down	0.024063
33389_at	down	0.024066
39905_i_at	down	0.024139
32782_r_at	up	0.024141
36369_at	up	0.024193
335_r_at	up	0.024272
37094_at	up	0.024294
33854_at	down	0.0243
37651_at	down	0.024336
32989_at	up	0.024341
40536_f_at	up	0.024357
38981_at	down	0.024383
325_s_at	up	0.024407
41574_at	down	0.024445
41865_at	down	0.024447
40275_at	up	0.024455
40971_at	down	0.024476
39868_at	up	0.024556
37284_at	up	0.024592
33994_g_at	up	0.024774
32705_at	up	0.024783
1757_i_at	up	0.024825
35199_at	down	0.024877

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chaperonin containing TCP1, subunit 6B (zeta 2)
ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 comple: subunit g
basic leucine zipper and W2 domains 1
muscleblind-like (Drosophila)
similar to RNA polymerase I transcription factor RRN3
nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
granzyme M (lymphocyte met-ase 1)
aldo-keto reductase family 1, member D1 (delta 4-3- ketosteroid-5-beta-reductase)
TRAF family member-associated NFKB activator
striatin, calmodulin binding protein
nuclear protein double minute 1
cytochrome P450, family 51, subfamily A, polypeptide 1
ADP-ribosylation factor GTPase activating protein 3
bullous pemphigoid antigen 1, 230/240kDa
polymerase I and transcript release factor
X-ray repair complementing defective repair in Chinese hamster cells 3
ATPase, H <sup>+</sup> transporting, lysosomal 34kDa, V1 subunit D
REST corepressor
regulatory factor X, 1 (influences HLA class II expression)
translation initiation factor IF2
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
pinin, desmosome associated protein
ATP synthase mitochondrial F1 complex assembly factor 2
karyopherin alpha 6 (importin alpha 7)
ankyrin repeat and SAM domain containing 1
poly(rC) binding protein 3
sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D
myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
cytochrome P450, family 3, subfamily A, polypeptide 7
cytochrome P450, family 3, subfamily A, polypeptide 7
KIAA0982 protein

31468_f_at	up	0.024961	glutamate receptor, metabotropic 1
36372_at	up	0.02499	hexokinase 3 (white cell)
41082_at	up	0.024994	ras homolog gene family, member N
32110_at	down	0.025003	KIAA0523 protein
32162_r_at	up	0.025004	
39746_at	down	0.025006	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa
39598_at	up	0.025046	gap junction protein, beta 1, 32kDa (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)
33815_at	down	0.025072	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)
1315_at	up	0.025082	ornithine decarboxylase antizyme 1
33368_at	down	0.025136	protease, serine, 15
33312_at	down	0.025138	crystallin, alpha A
922_at	up	0.025139	protein phosphatase 2 (formerly 2A), regulatory subunit / (PR 65), alpha isoform
33234_at	down	0.02522	KIAA0117 protein
39383_at	up	0.025256	adenylate cyclase 6
36375_at	up	0.025313	outer dense fiber of sperm tails 1
32039_at	down	0.025325	adaptor-related protein complex 3, beta 1 subunit
1397_at	down	0.025353	mitogen-activated protein kinase kinase kinase 11
36599_at	down	0.02539	malic enzyme 2, NAD(+)-dependent, mitochondrial
39316_at	up	0.025404	RAB40C, member RAS oncogene family
41194_at	down	0.025416	signal recognition particle 14kDa (homologous Alu RNA binding protein)
41088_at	down	0.02547	abhydrolase domain containing 2
38869_at	up	0.025484	KIAA1069 protein
33885_at	down	0.025514	KIAA0907 protein
32955_at	down	0.025531	hypothetical protein HSPC132
36670_at	up	0.025564	autoantigen
33630_s_at	up	0.025599	spectrin, beta, non-erythrocytic 2
36930_at	down	0.02563	nucleolar GTPase
33459_at	up	0.025662	
40121_at	down	0.02568	huntingtin interacting protein 2
37562_at	up	0.025703	protocadherin 1 (cadherin-like 1)
37658_at	up	0.025706	growth arrest-specific 6
32880_at	up	0.02574	secretoglobulin, family 1D, member 2
40094_r_at	up	0.025791	Lutheran blood group (Auberger b antigen included)
1849_s_at	down	0.025971	retinoblastoma binding protein 1
34342_s_at	up	0.025976	secreted phosphoprotein 1 (osteopontin, bone sialoprotein, early T-lymphocyte activation 1)
39679_at	up	0.025985	aquaporin 2 (collecting duct)
41133_at	down	0.02604	Ras-GTPase-activating protein SH3-domain-binding protein
40718_at	up	0.026084	cathepsin W (lymphopain)

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33300_at	up	0.0261	galanin receptor 3
40029_at	up	0.026123	EGF-like-domain, multiple 3
41239_r_at	down	0.026185	cathepsin S
33363_at	up	0.026322	JTV1 gene
40980_at	up	0.026323	helicase with SNF2 domain 1
37280_at	up	0.026356	MAD, mothers against decapentaplegic homolog 1 (Drosophila)
37059_at	up	0.026359	glucokinase (hexokinase 4) regulatory protein
34304_s_at	down	0.02639	spermidine/spermine N1-acetyltransferase
41750_at	down	0.026432	protein disulfide isomerase-related protein
34026_at	up	0.026444	
35828_at	up	0.026456	cysteine-rich protein 2
34655_at	up	0.02651	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)
35955_at	up	0.026544	cytochrome c-like antigen
33930_at	down	0.026608	chromosome 14 open reading frame 163
40664_at	up	0.026615	brain-specific angiogenesis inhibitor 3
34110_g_at	up	0.026639	proline dehydrogenase (oxidase) 1
36271_at	up	0.026668	KIAA1024 protein
1498_at	up	0.026683	zeta-chain (TCR) associated protein kinase 70kDa
1647_at	down	0.026835	IQ motif containing GTPase activating protein 2
35069_at	up	0.026876	hypothetical protein similar to preferentially expressed antigen of melanoma
35135_at	down	0.026898	hypothetical protein MGC10471
34099_f_at	down	0.02691	nucleosome assembly protein 1-like 1
33861_at	down	0.02691	CCR4-NOT transcription complex, subunit 2
39720_g_at	up	0.026932	zona pellucida glycoprotein 3 (sperm receptor)
249_at	up	0.026938	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
35013_at	up	0.026947	lipopolysaccharide binding protein
40164_at	up	0.027001	Rho GDP dissociation inhibitor (GDI) alpha
41828_at	down	0.027034	methyl-CpG binding domain protein 1
33658_at	down	0.027078	zinc finger protein 124 (HZF-16)
32665_at	down	0.027087	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform
35734_at	down	0.027114	ARP2 actin-related protein 2 homolog (yeast)
36753_at	down	0.027141	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4
35087_at	down	0.027142	
34887_at	down	0.027168	radixin
36048_at	down	0.027245	zinc finger protein 318
728_at	up	0.027264	
33030_at	up	0.027277	histone 1, H1d
35818_at	down	0.027352	cytochrome c, somatic
1171_s_at	up	0.027371	

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32508_at	down	0.027482	HBxAg transactivated protein 2
37758_s_at	up	0.027495	transcription factor Dp-1
31474_r_at	down	0.027515	tankyrase, TRF 1-interacting ankyrin-related ADP-ribose polymerase
31716_at	up	0.027701	protocadherin 1 (cadherin-like 1)
39377_at	down	0.027712	mitochondrial ribosomal protein S27
32833_at	down	0.027752	CDC-like kinase 1
36702_at	up	0.027768	T-box 19
222_at	up	0.027825	exostoses (multiple) 1
35378_at	up	0.027861	luteinizing hormone beta polypeptide
37399_at	up	0.027864	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)
41249_at	down	0.027899	NAD kinase
37419_g_at	up	0.027936	POU domain, class 2, transcription factor 2
36598_s_at	up	0.028084	inositol polyphosphate phosphatase-like 1
36400_at	up	0.028084	
34946_at	down	0.028102	immunoglobulin superfamily, member 6
39568_g_at	up	0.028143	aquaporin 7
33847_s_at	down	0.028151	cyclin-dependent kinase inhibitor 1B (p27, Kip1)
33774_at	down	0.028182	caspase 8, apoptosis-related cysteine protease
723_s_at	down	0.028219	
40852_at	down	0.028237	tudor repeat associator with PCTAIRE 2
32315_at	down	0.02827	ribosomal protein S24
32017_at	up	0.028338	par-6 partitioning defective 6 homolog beta (C. elegans)
32254_at	up	0.02834	vesicle-associated membrane protein 2 (synaptobrevin 2)
32923_r_at	up	0.028392	synapsin I
38515_at	up	0.028404	bone morphogenetic protein 7 (osteogenic protein 1)
32012_at	up	0.02841	pecanex homolog (Drosophila)
39510_r_at	down	0.028439	programmed cell death 4 (neoplastic transformation inhibitor)
34077_at	up	0.028472	chemokine (C-X-C motif) receptor 3
41198_at	up	0.028513	granulin
32649_at	down	0.028531	transcription factor 7 (T-cell specific, HMG-box)
40968_at	up	0.028537	suppressor of cytokine signaling 3
1587_at	up	0.028563	retinoic acid receptor, gamma
38583_at	down	0.028622	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2
1859_s_at	up	0.028629	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)
36244_at	up	0.028641	zinc finger protein 239
39346_at	down	0.028649	KH domain containing, RNA binding, signal transduction associated 1
40607_at	down	0.028666	dihydropyrimidinase-like 2
40659_at	up	0.02869	nuclear receptor subfamily 4, group A, member 3

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37112_at	down	0.028745	chromosome 6 open reading frame 32
812_at	down	0.028758	protein phosphatase 1, regulatory (inhibitor) subunit 2
35095_r_at	down	0.028761	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3
35178_at	up	0.028823	WNT inhibitory factor 1
40655_at	up	0.028827	huntingtin-associated protein interacting protein (duo)
38082_at	down	0.02887	KIAA0650 protein
41465_at	down	0.028906	zinc finger protein 148 (pHZ-52)
39932_at	down	0.028952	
35417_at	up	0.028976	cubilin (intrinsic factor-cobalamin receptor)
40893_at	down	0.029072	succinate-CoA ligase, ADP-forming, beta subunit
40941_at	up	0.029096	VAMP (vesicle-associated membrane protein)-associate protein B and C
40351_at	down	0.029119	guanine nucleotide binding protein (G protein), beta polypeptide 3
988_at	down	0.02912	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)
34906_g_at	up	0.029139	glutamate receptor, ionotropic, kainate 5
35900_at	up	0.029265	artemin
33138_at	up	0.029266	myeloid leukemia factor 1
36722_s_at	up	0.029339	hepatocyte nuclear factor 4, alpha
38025_r_at	up	0.029343	rap2 interacting protein x
1271_g_at	up	0.029435	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)
39278_at	up	0.029472	transglutaminase 4 (prostate)
766_at	up	0.029553	lectin, galactoside-binding, soluble, 9 (galectin 9)
36335_at	up	0.029597	butyrophilin, subfamily 1, member A1
38270_at	down	0.02961	poly (ADP-ribose) glycohydrolase
258_at	up	0.029653	lymphotoxin alpha (TNF superfamily, member 1)
38289_r_at	up	0.029684	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)
37336_at	down	0.029708	UBX domain containing 2
35252_at	down	0.02973	KIAA0528 gene product
1102_s_at	down	0.0298	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
38041_at	down	0.029812	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)
36330_at	up	0.029865	cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotransferase)
525_g_at	down	0.029867	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
41458_at	up	0.029904	KIAA0467 protein
32466_at	up	0.029925	ribosomal protein L41
1659_s_at	down	0.029946	Ras homolog enriched in brain 2



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35460_at	up	0.029947	G protein-coupled receptor 4
223_at	down	0.02995	ubiquitin-conjugating enzyme E2L 3
34411_at	down	0.030124	3'-phosphoadenosine 5'-phosphosulfate synthase 1
1632_at	up	0.030132	
33051_at	up	0.030141	gamma-aminobutyric acid (GABA) receptor, rho 1
1441_s_at	down	0.030183	tumor necrosis factor receptor superfamily, member 6
32946_r_at	up	0.030222	mannose-binding lectin (protein C) 2, soluble (opsonic defect)
35258_f_at	down	0.030223	splicing factor, arginine/serine-rich 2, interacting protein
36677_at	down	0.030277	coatomer protein complex, subunit beta 2 (beta prime)
41463_at	up	0.030285	hypothetical protein FLJ38984
36636_at	down	0.030335	ornithine aminotransferase (gyrate atrophy)
39778_at	up	0.030338	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
41000_at	down	0.03037	checkpoint suppressor 1
32065_at	up	0.030391	cAMP responsive element modulator
34372_at	down	0.030409	upstream regulatory element binding protein 1
35424_g_at	up	0.030417	glutamate receptor, metabotropic 5
36835_at	down	0.030439	protein kinase C-like 2
39920_r_at	up	0.030491	C1q-related factor
35408_i_at	down	0.030498	GIOT-2 for gonadotropin inducible transcription represso 2
31878_at	down	0.030618	ATP-binding cassette, sub-family F (GCN20), member 2
38613_at	up	0.03062	putative cyclin G1 interacting protein
41780_at	down	0.03067	protein tyrosine phosphatase, receptor type, f polypeptid (PTPRF), interacting protein (liprin), alpha 1
33369_at	down	0.030743	sterol-C4-methyl oxidase-like
34783_s_at	down	0.030757	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)
35212_at	down	0.03079	ring finger protein 139
38507_at	up	0.030852	cytochrome P450, family 2, subfamily D, polypeptide 6
33163_r_at	down	0.030898	glutamate-cysteine ligase, modifier subunit
36798_g_at	up	0.030948	sialophorin (gpL115, leukosialin, CD43)
39132_at	down	0.031073	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
34534_at	up	0.031122	opioid receptor, mu 1
40074_at	down	0.031215	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
38293_s_at	up	0.031221	homeo box D3

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33237_at	down	0.031222	RNA helicase
36233_at	up	0.031254	3'-phosphoadenosine 5'-phosphosulfate synthase 2
32145_at	up	0.031307	adducin 1 (alpha)
39499_s_at	up	0.031346	par-3 partitioning defective 3 homolog (C. elegans)
36684_at	down	0.031356	adenosylmethionine decarboxylase 1
34760_at	down	0.031481	C-type lectin BIMLEC precursor
40126_at	up	0.031527	paired mesoderm homeo box 1
31349_at	up	0.031545	DNA-binding protein amplifying expression of surfactant protein B
1007_s_at	up	0.031546	discoïdin domain receptor family, member 1
37185_at	up	0.031584	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2
32100_r_at	up	0.031585	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)
34381_at	down	0.031631	cytochrome c oxidase subunit VIc
36285_at	up	0.031708	potassium inwardly-rectifying channel, subfamily J, member 4
171_at	down	0.031713	von Hippel-Lindau binding protein 1
39659_at	down	0.031715	Ts translation elongation factor, mitochondrial
37289_at	up	0.031818	cadherin 8, type 2
36218_g_at	up	0.031859	serine/threonine kinase 38
31410_at	up	0.031863	tumor necrosis factor receptor superfamily, member 13B
35387_r_at	up	0.031917	acetylcholinesterase (YT blood group)
33598_r_at	down	0.031933	cold autoinflammatory syndrome 1
38435_at	down	0.031934	peroxiredoxin 4
36510_at	down	0.031942	general transcription factor IIF, polypeptide 2, 30kDa
41048_at	down	0.031992	phorbol-12-myristate-13-acetate-induced protein 1
38441_s_at	down	0.03202	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)
39483_s_at	down	0.032042	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
31889_at	up	0.032073	melan-A
39443_s_at	down	0.032107	cytochrome c oxidase subunit Vb
40172_g_at	up	0.032138	frequently rearranged in advanced T-cell lymphomas 2
36580_at	down	0.032164	hypothetical protein FLJ13910
1140_at	down	0.032164	Integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
37877_at	up	0.032166	DKFZP564C103 protein
38402_at	down	0.032188	lysosomal-associated membrane protein 2
39037_at	down	0.032197	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2
34830_at	up	0.032228	hypothetical protein DKFZp564K0822
32313_at	up	0.032235	tropomyosin 2 (beta)

36332_at	up	0.032309	arylalkylamine N-acetyltransferase
36979_at	up	0.032388	solute carrier family 2 (facilitated glucose transporter), member 3
32892_at	up	0.032417	ribosomal protein S6 kinase, 90kDa, polypeptide 2
1818_at	down	0.032454	
38040_at	down	0.032494	splicing factor 30, survival of motor neuron-related
31771_at	up	0.032514	
37006_at	down	0.032531	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
35310_at	up	0.032585	
2090_i_at	up	0.032631	
36647_at	down	0.032661	hypothetical protein FLJ10326
35259_s_at	down	0.032688	splicing factor, arginine/serine-rich 2, interacting protein
1105_s_at	up	0.032709	T cell receptor beta locus
31904_at	up	0.03274	phosphodiesterase 2A, cGMP-stimulated
40207_g_at	down	0.032759	chymotrypsin-like
38397_at	down	0.03281	polymerase (DNA-directed), delta 4
38681_at	down	0.03289	eukaryotic translation initiation factor 3, subunit 6 48kDa
37164_at	up	0.032937	Rhesus blood group, D antigen
37944_at	down	0.032989	GTP cyclohydrolase 1 (dopa-responsive dystonia)
34091_s_at	up	0.033014	vimentin
34008_at	up	0.033133	RAS (RAD and GEM)-like GTP-binding
39879_s_at	up	0.033144	hypothetical protein FLJ10120
37178_at	up	0.03329	hypothetical protein BC017169
36444_s_at	down	0.033356	chemokine (C-C motif) ligand 23
33574_at	up	0.033458	chromosome 6 open reading frame 10
39725_at	down	0.033516	RNA-binding region (RNP1, RRM) containing 2
33871_s_at	up	0.033547	folate receptor 2 (fetal)
891_at	down	0.033587	YY1 transcription factor
37514_s_at	up	0.033701	mannan-binding lectin serine protease 2
32666_at	up	0.033716	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
32498_at	up	0.033761	glutamate receptor, metabotropic 2
33967_at	up	0.033788	major histocompatibility complex, class II, DO alpha
34280_at	up	0.033821	gamma-aminobutyric acid (GABA) A receptor, epsilon
32178_r_at	down	0.033864	synaptosomal-associated protein, 23kDa
39701_at	up	0.033899	paternally expressed 3
38715_at	up	0.033904	glycophorin B (includes Ss blood group)
40144_at	down	0.033918	protein tyrosine phosphatase, non-receptor type substrate 1
41830_at	down	0.033922	KIAA0494 gene product

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35211_at	up	0.034035	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha
38123_at	down	0.034045	chromosome 10 open reading frame 7
39341_at	up	0.034163	thyroid hormone receptor interactor 6
33651_at	up	0.034184	aquaporin 8
41549_s_at	down	0.034205	adaptor-related protein complex 1, sigma 2 subunit
40897_at	down	0.034209	phosphodiesterase 6A, cGMP-specific, rod, alpha
37586_at	up	0.034298	zinc finger protein 142 (clone pHZ-49)
32175_at	down	0.034333	CDC10 cell division cycle 10 homolog (S. cerevisiae)
34368_at	down	0.034371	histone deacetylase 2
40859_at	down	0.034403	nuclear protein UKp68
35588_at	down	0.034495	zinc finger protein 443
33977_at	up	0.034609	growth factor independent 1
623_s_at	down	0.034643	RAB2, member RAS oncogene family
41747_s_at	down	0.034656	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)
33381_at	down	0.034676	nuclear receptor coactivator 3
35367_at	down	0.03477	lectin, galactoside-binding, soluble, 3 (galectin 3)
1964_g_at	up	0.034805	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
41637_at	up	0.034911	dexamethasone-induced transcript
39888_at	up	0.034927	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5
38847_at	up	0.034942	maternal embryonic leucine zipper kinase
36897_at	up	0.034982	megalencephalic leukoencephalopathy with subcortical cysts 1
37984_s_at	down	0.035019	ADP-ribosylation factor 6
41505_r_at	down	0.035043	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
1292_at	up	0.035215	dual specificity phosphatase 2
35505_at	up	0.035231	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1
38664_at	down	0.035232	craniofacial development protein 1
35572_f_at	down	0.035287	zinc finger protein 253
32281_at	up	0.035303	sorting nexin 15
32478_f_at	down	0.035339	
32094_at	up	0.035363	carbohydrate (chondroitin 6) sulfotransferase 3
38597_f_at	up	0.035398	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
41446_f_at	up	0.035415	RNA helicase-related protein
38711_at	down	0.035439	cytoplasmic linker associated protein 2
1017_at	down	0.035486	
39288_at	up	0.035547	nectin-like protein 1

710_at	up	0.035599	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proli 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)
36690_at	down	0.03562	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
33424_at	down	0.035644	ribophorin I
943_at	down	0.035681	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)
39822_s_at	down	0.035691	growth arrest and DNA-damage-inducible, beta
41768_at	down	0.035716	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
40773_at	up	0.03575	myosin, light polypeptide 5, regulatory
35720_at	down	0.035787	KIAA0893 protein
40151_s_at	down	0.035808	peroxisome receptor 1
1640_at	down	0.035835	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)
41054_at	up	0.035852	KIAA0290 protein
37724_at	down	0.0359	v-myc myelocytomatosis viral oncogene homolog (avian)
38654_at	down	0.035915	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
34251_at	up	0.035965	homeo box B5
36974_at	down	0.036018	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)
34197_at	up	0.036025	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
39092_at	down	0.036029	histone H2A.F/Z variant
38972_at	down	0.036149	hypothetical protein BC013764
34060_g_at	up	0.036265	Pvt1 oncogene homolog, MYC activator (mouse)
32898_at	up	0.036315	actin like protein
40945_at	up	0.03632	TGFB inducible early growth response 2
AFFX-BioDn- 3_st	up	0.036336	
37568_at	up	0.036344	
37591_at	up	0.036353	uncoupling protein 2 (mitochondrial, proton carrier)
35991_at	down	0.036357	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)
40193_at	up	0.036372	enolase 2, (gamma, neuronal)
39885_at	down	0.036385	putative dimethyladenosine transferase
239_at	up	0.036478	cathepsin D (lysosomal aspartyl protease)
41279_f_at	up	0.03657	mitogen-activated protein kinase 8 interacting protein 1
32630_f_at	down	0.03659	butyrophilin, subfamily 3, member A1
38985_at	down	0.036653	leptin receptor overlapping transcript-like 1
41510_s_at	down	0.036688	heat shock 70kDa protein 9B (mortalin-2)

39744_at	down	0.036695	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3
41561_s_at	down	0.03671	intraflagellar transport protein IFT20
37482_at	up	0.036796	aldo-keto reductase family 1, member B10 (aldose reductase)
36968_s_at	down	0.036823	Opa-interacting protein 2
34750_r_at	down	0.036851	zinc finger and BTB domain containing 1
1274_s_at	up	0.036896	cell division cycle 34
35713_at	up	0.036927	Fanconi anemia, complementation group C
37643_at	down	0.036948	tumor necrosis factor receptor superfamily, member 6
34364_at	up	0.036957	peptidylprolyl isomerase E (cyclophilin E)
760_at	down	0.037036	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
34965_at	up	0.037053	cystatin F (leukocystatin)
32503_at	down	0.037099	sorting nexin 27
37192_at	up	0.037113	erythrocyte membrane protein band 4.9 (dematin)
39613_at	down	0.037219	mannosidase, alpha, class 1A, member 1
975_at	up	0.03724	serine/threonine kinase 18
37673_at	down	0.037261	neutral sphingomyelinase (N-SMase) activation associated factor
34191_at	down	0.037275	
1450_g_at	down	0.03728	proteasome (prosome, macropain) subunit, alpha type, 4
33154_at	down	0.037299	proteasome (prosome, macropain) subunit, beta type, 4
39637_at	down	0.037323	solute carrier family 26 (sulfate transporter), member 2
33781_s_at	up	0.037374	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)
38364_at	down	0.037386	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)
34902_at	up	0.03739	KIAA0492 protein
36516_at	up	0.037461	zinc finger protein ZFP100
949_s_at	down	0.037476	proteasome (prosome, macropain) 26S subunit, ATPase 6
36777_at	up	0.037482	DNA segment on chromosome 12 (unique) 2489 expressed sequence
38764_at	down	0.037533	
1231_at	down	0.037551	ubiquitin-conjugating enzyme E2B (RAD6 homolog)
33765_at	up	0.037599	chemokine (C-X-C motif) ligand 2
34089_at	up	0.037666	KIAA1030 protein
39104_at	up	0.037676	
36311_at	up	0.037683	phosphodiesterase 1A, calmodulin-dependent
31636_s_at	up	0.037708	solute carrier family 18 (vesicular acetylcholine), member 3
32029_at	up	0.037719	3-phosphoinositide dependent protein kinase-1
37107_at	down	0.037821	protein phosphatase 1D magnesium-dependent, delta isoform

36780_at	up	0.037836	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)
39915_at	up	0.037879	transient receptor potential cation channel, subfamily M, member 2
38895_i_at	up	0.038008	neutrophil cytosolic factor 4, 40kDa
31689_at	down	0.038009	DKFZP564G092 protein
35652_g_at	down	0.038037	mitogen-activated protein kinase kinase kinase 4
37483_at	down	0.038043	histone deacetylase 9
36016_at	up	0.038044	cortistatin
36568_at	up	0.03806	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7
31411_at	up	0.038106	variable charge, Y chromosome, 2
314_at	down	0.038139	phosphatidylinositol glycan, class B
33761_s_at	up	0.038262	KIAA0493 protein
32983_at	up	0.038292	adrenergic, alpha-1B-, receptor
40143_at	down	0.038345	KIAA0140 gene product
37671_at	down	0.038399	laminin, alpha 4
38727_at	down	0.03847	multiple coagulation factor deficiency protein 2
35535_f_at	up	0.038485	KIAA0565 gene product
35762_at	down	0.038526	KIAA0483 protein
1260_s_at	up	0.038541	glutathione S-transferase A2
35539_at	up	0.038541	interphotoreceptor matrix proteoglycan 1
33067_at	up	0.038554	histone 1, H1a
33450_at	up	0.038556	actin-like 6
34795_at	up	0.038587	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
35353_at	down	0.038672	proteasome (prosome, macropain) 26S subunit, ATPase 2
390_at	up	0.038847	chemokine (C-C motif) receptor 4
38160_at	down	0.038867	lymphocyte antigen 75
962_at	up	0.038972	BMX non-receptor tyrosine kinase
36347_f_at	up	0.039084	histone 1, H2bn
35221_at	down	0.039152	purine-rich element binding protein A
32043_at	up	0.039176	stanniocalcin 2
1940_at	down	0.039252	v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog
39338_at	down	0.039273	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
40840_at	up	0.039302	peptidylprolyl isomerase F (cyclophilin F)
422_s_at	up	0.03932	MAX protein
32196_at	up	0.039333	TBP-interacting protein
41699_f_at	down	0.039349	bromodomain containing 1
31826_at	up	0.039468	KIAA0674 protein
37309_at	up	0.03947	ras homolog gene family, member A

35262_at	up	0.039475	integrin beta 4 binding protein
2089_s_at	up	0.039507	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
31798_at	up	0.039562	trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed in)
39068_at	up	0.039709	protein phosphatase 2, regulatory subunit B (B56), delta isoform
40668_s_at	up	0.039712	CD6 antigen
38405_at	down	0.03972	fragile X mental retardation, autosomal homolog 1
37664_at	up	0.039744	developmentally regulated GTP binding protein 2
39908_at	up	0.039777	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa
32209_at	up	0.03978	Mouse Mammary Tumor Virus Receptor homolog 1
37885_at	up	0.039796	hypothetical protein AF038169
38454_g_at	down	0.039796	intercellular adhesion molecule 2
37007_at	down	0.039799	tumor differentially expressed 1
697_f_at	up	0.039946	
34643_at	up	0.039976	ribosomal protein S4, X-linked
31331_at	up	0.040002	surfactant protein A binding protein
1726_at	up	0.040012	
33208_at	down	0.040098	DnaJ (Hsp40) homolog, subfamily C, member 3
38220_at	down	0.040129	dihydropyrimidine dehydrogenase
36986_at	up	0.040158	lysophospholipase II
41429_at	up	0.040222	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform
34460_at	up	0.040229	benzodiazapine receptor (peripheral) associated protein
762_f_at	up	0.040254	histone 1, H4i
31860_at	down	0.040289	chromosome 17 open reading frame 35
39111_s_at	down	0.040343	peptidylprolyl isomerase (cyclophilin)-like 2
40102_at	down	0.040375	oxysterol binding protein-like 2
35719_at	down	0.040521	pleckstrin homology domain containing, family E (with leucine rich repeats) member 1
34605_at	up	0.040586	activating transcription factor 7
37324_at	down	0.040601	transferrin receptor (p90, CD71)
41692_at	down	0.040613	synaptojanin 1
39345_at	down	0.040629	Niemann-Pick disease, type C2
40612_at	down	0.040677	KIAA1117 protein
38690_at	down	0.040763	chromosome 3 open reading frame 4
41046_s_at	up	0.040853	zinc finger protein 261
38450_at	down	0.040905	Sjogren syndrome antigen B (autoantigen La)
31461_at	up	0.041106	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4, pseudogene
32087_at	down	0.041149	heat shock transcription factor 2
317_at	up	0.041156	legumain
32204_at	up	0.04122	phosphodiesterase 6G, cGMP-specific, rod, gamma
37242_at	down	0.041221	hypothetical protein MGC5149
35163_at	down	0.041239	KIAA1041 protein



34047_at	up	0.041244	ovo-like 1(Drosophila)
292_s_at	down	0.041287	
37889_at	up	0.041327	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)
706_at	down	0.04142	
1946_at	up	0.041472	Wilms tumor associated protein
34067_at	up	0.041485	type II transmembrane serine protease 6
41698_at	up	0.041503	solute carrier family 9 (sodium/hydrogen exchanger), isoform 8
36325_at	up	0.041595	crystallin, beta A1
39103_s_at	up	0.041671	
39319_at	down	0.041707	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)
39621_at	up	0.04171	KIAA0459 protein
32830_g_at	down	0.041825	translocase of inner mitochondrial membrane 17 homolog A (yeast)
34816_at	down	0.041866	E1A binding protein p400
32736_at	up	0.041867	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
33553_r_at	down	0.041915	chemokine (C-C motif) receptor 6
1521_at	down	0.041957	non-metastatic cells 1, protein (NM23A) expressed in
35290_at	down	0.041996	hypothetical protein FLJ31657
34430_at	up	0.042007	glutamic-pyruvate transaminase (alanine aminotransferase)
34376_at	up	0.042019	protein kinase (cAMP-dependent, catalytic) inhibitor gamma
1323_at	down	0.042034	ubiquitin B
1537_at	up	0.042061	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
33008_at	up	0.042078	olfactory receptor, family 7, subfamily E, member 24 pseudogene
32918_at	up	0.0422	
39027_at	down	0.042311	cytochrome c oxidase subunit IV isoform 1
41436_at	down	0.042331	zinc finger protein 198
34864_at	up	0.042446	hypothetical protein CGI-57
39503_s_at	up	0.042509	dihydropyrimidinase-like 4
35709_at	down	0.042524	hypothetical protein FLJ11149
37011_at	down	0.04259	allograft inflammatory factor 1
31439_f_at	up	0.042596	Rhesus blood group, CcEe antigens
39557_at	down	0.042673	
40019_at	down	0.042779	ecotropic viral integration site 2B
32499_at	up	0.04278	Rho GDP dissociation inhibitor (GDI) gamma
35854_at	down	0.042925	solute carrier family 18 (vesicular monoamine), member 2
34840_at	down	0.042926	
37936_at	down	0.043001	PRP4 pre-mRNA processing factor 4 homolog (yeast)

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30099_at	down	0.043002	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
39530_at	up	0.043068	enigma (LIM domain protein)
40926_at	up	0.043095	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
AFFX-BioB-3_at	up	0.043174	
34135_at	up	0.043181	
31544_at	up	0.043193	forkhead box I1
38276_at	down	0.043244	nuclear factor of kappa light polypeptide gene enhancer B-cells inhibitor, epsilon
35166_at	down	0.043337	Down syndrome critical region gene 3
41394_at	up	0.043359	phospholipase D2
33339_g_at	down	0.043366	signal transducer and activator of transcription 1, 91kDa
33317_at	down	0.043374	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)
33920_at	up	0.043398	diaphanous homolog 1 (Drosophila)
39897_at	down	0.043457	splicing factor YT521-B
39739_at	down	0.043459	nascent-polypeptide-associated complex alpha polypeptide
40596_at	up	0.04355	Treacher Collins-Franceschetti syndrome 1
39794_at	down	0.043575	ubiquitin specific protease 8
41153_f_at	down	0.043582	catenin (cadherin-associated protein), alpha 1, 102kDa
38503_at	up	0.043583	aldehyde dehydrogenase 1 family, member B1
40220_at	down	0.043623	HMBA-inducible
31752_at	up	0.043695	hypothetical protein FLJ23142
36174_at	down	0.043725	MARCKS-like protein
36197_at	down	0.043728	chitinase 3-like 1 (cartilage glycoprotein-39)
1692_s_at	up	0.043818	GDNF family receptor alpha 2
35513_r_at	up	0.043851	Rho family guanine-nucleotide exchange factor
31566_at	up	0.043873	
32161_at	down	0.043989	seven in absentia homolog 1 (Drosophila)
34277_at	up	0.044051	carbonic anhydrase XI
38808_at	up	0.044055	adhesion regulating molecule 1
40864_at	down	0.044105	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
35388_at	up	0.044116	LIM homeobox protein 1
251_at	down	0.04425	calcium/calmodulin-dependent protein kinase I
34792_at	down	0.044292	S-adenosylhomocysteine hydrolase-like 1
32007_at	up	0.044325	
39163_at	down	0.04434	likely homolog of rat kinase D-interacting substance of 220 kDa
31676_at	up	0.044351	zinc finger protein 208
38323_at	down	0.044372	carboxypeptidase, vitellogenic-like
32028_at	up	0.044373	phosphomannomutase 2
34959_at	up	0.044378	Fc fragment of IgE, low affinity II, receptor for (CD23A)
35193_at	down	0.044416	chromosome condensation 1-like

33415_at	down	0.044429	non-metastatic cells 2, protein (NM23B) expressed in
37356_r_at	down	0.044508	vesicle docking protein p115
33950_g_at	up	0.044544	corticotropin releasing hormone receptor 2
36913_at	down	0.044573	stem-loop (histone) binding protein
41559_at	down	0.044597	KIAA1201 protein
38187_at	down	0.044461	N-acetyltransferase 1 (arylamine N-acetyltransferase)
40972_at	down	0.044616	v-akt murine thymoma viral oncogene homolog 2
595_at	down	0.04463	tumor necrosis factor, alpha-induced protein 3
34693_at	down	0.044662	sialyltransferase
34870_at	up	0.044673	LIM domain binding 3
1116_at	up	0.044741	CD19 antigen
36490_s_at	up	0.044883	phosphoribosyl pyrophosphate synthetase 1
37696_at	down	0.044938	voltage-dependent anion channel 2
32369_at	up	0.044951	serum amyloid A4, constitutive
36537_at	down	0.044967	Rho-specific guanine nucleotide exchange factor p114
279_at	down	0.044968	nuclear receptor subfamily 4, group A, member 1
35379_at	up	0.045025	collagen, type IX, alpha 1
1573_at	up	0.045053	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)
38247_at	down	0.045143	coagulation factor II (thrombin) receptor-like 1
39763_at	up	0.045196	hemopexin
1093_at	down	0.045205	protein phosphatase 2 (formerly 2A), regulatory subunit / (PR 65), beta isoform
36238_at	up	0.045459	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7
31434_at	up	0.045471	
36177_at	down	0.04549	translin
39270_at	up	0.045516	CD209 antigen-like
32547_at	down	0.045552	mannose-6-phosphate receptor (cation dependent)
32948_at	up	0.045614	Usher syndrome 2A (autosomal recessive, mild)
39028_at	down	0.045662	karyopherin (importin) beta 3
34634_s_at	up	0.045678	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)
38544_at	up	0.04577	inhibin, alpha
41597_s_at	down	0.045846	SEC22 vesicle trafficking protein-like 1 (S. cerevisiae)
38144_at	up	0.045854	hypothetical protein DKFZp667B1218
39758_f_at	up	0.045944	lysosomal-associated membrane protein 1
38436_at	down	0.045972	KIAA0252 protein
32143_at	up	0.045998	odd-skipped-related 2A protein
37391_at	down	0.046076	cathepsin L
41860_at	down	0.046107	hypothetical protein BC015148
1913_at	down	0.046111	cyclin G2
244_at	down	0.046131	heat shock transcription factor 1
38746_at	up	0.046186	integrin, beta 4

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35896_at	up	0.046222	DKFZp434P211 protein
40115_at	down	0.046251	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex gamma polypeptide 1
35251_at	down	0.046264	human immunodeficiency virus type 1 enhancer binding protein 1
1678_g_at	up	0.046272	insulin-like growth factor binding protein 5
32389_at	up	0.046313	RNA, U2 small nuclear
40951_at	up	0.04634	BTG3 associated nuclear protein
33708_at	up	0.046346	prostate cancer overexpressed gene 1
41530_at	down	0.046412	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)
40049_at	down	0.046435	death-associated protein kinase 1
37276_at	down	0.04647	IQ motif containing GTPase activating protein 2
37512_at	up	0.046491	3-hydroxysteroid epimerase
33862_at	up	0.046504	phosphatidic acid phosphatase type 2B
1427_g_at	down	0.046519	Src-like-adaptor
34367_at	up	0.04653	phosphoglycerate dehydrogenase
38823_s_at	down	0.0466	serine/threonine kinase 17a (apoptosis-inducing)
1257_s_at	up	0.046621	quiescin Q6
37237_at	up	0.046666	adaptor-related protein complex 3, mu 2 subunit
38747_at	up	0.046695	CD34 antigen
35038_at	up	0.046799	myosin binding protein C, cardiac
39046_at	down	0.046853	histone H2A.F/Z variant
35109_at	up	0.046897	neurofascin
34586_s_at	up	0.046906	distal-less homeo box 2
37522_r_at	down	0.046935	nucleolar cysteine-rich protein
40160_at	down	0.046944	POM121 membrane glycoprotein (rat)
40791_at	up	0.046947	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa
31357_at	up	0.046987	TEA domain family member 3
33808_at	up	0.046995	DKFZP586B0923 protein
40831_at	down	0.047033	acidic 82 kDa protein mRNA
37938_at	down	0.047074	postmeiotic segregation increased 2-like 9
35858_at	up	0.047084	hypothetical gene supported by AF038182; BC009203
33466_at	up	0.047098	
783_at	down	0.047127	WW domain-containing protein 1
36232_at	up	0.047127	fibroblast growth factor 13
33947_at	up	0.047147	G protein-coupled receptor 3
40317_at	up	0.047216	amiloride-sensitive cation channel 1, neuronal (degenerative)
39782_at	down	0.047224	nuclear DNA-binding protein
35829_at	up	0.04723	immunoglobulin superfamily, member 4
38193_at	up	0.047282	immunoglobulin kappa constant
31510_s_at	down	0.047301	H3 histone, family 3B (H3.3B)

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41303_r_at	down	0.047306	hypothetical protein dJ465N24.2.1
37831_at	up	0.047318	KIAA0545 protein
38138_at	up	0.047335	S100 calcium binding protein A11 (calgizzarin)
32852_at	up	0.047348	thioredoxin 2
31408_at	up	0.047356	retinal pigment epithelium-derived rhodopsin homolog
38758_at	up	0.047434	PDGFA associated protein 1
37905_r_at	up	0.047444	
41572_r_at	down	0.047457	v-rel reticuloendotheliosis viral oncogene homolog (avian
35294_at	down	0.047527	Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro)
40494_at	up	0.047561	death effector domain containing
37510_at	down	0.047611	syntaxin 8
39056_at	down	0.047621	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
38527_at	down	0.047648	non-POU domain containing, octamer-binding
37713_at	up	0.047659	aminoacylase 1
39755_at	up	0.047681	X-box binding protein 1
31816_at	up	0.047754	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)
31381_at	up	0.048043	peptidoglycan recognition protein
32240_at	up	0.048048	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5
40105_at	down	0.048138	methylmalonyl Coenzyme A mutase
35311_at	down	0.048157	cellular repressor of E1A-stimulated genes
39122_at	up	0.048174	glucose phosphate isomerase
37640_at	down	0.048183	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhar syndrome)
36313_at	down	0.048202	ecotropic viral integration site 2A
32052_at	up	0.048233	hemoglobin, beta
32928_at	up	0.048347	POU domain, class 2, transcription factor 3
40519_at	down	0.048417	protein tyrosine phosphatase, receptor type, C
40910_at	down	0.048437	capping protein (actin filament) muscle Z-line, alpha 1
39139_at	down	0.048449	signal peptidase complex (18kD)
35184_at	down	0.048653	hypothetical protein MGC23401
38319_at	down	0.048706	CD3D antigen, delta polypeptide (TIT3 complex)
32716_at	up	0.048729	diacylglycerol kinase, alpha 80kDa
37931_at	up	0.048751	centromere protein B, 80kDa
41435_at	up	0.048872	protein tyrosine phosphatase, receptor type, f polypeptid (PTPRF), interacting protein (liprin), alpha 3
40833_r_at	down	0.048945	lamina-associated polypeptide 1B
34292_at	down	0.048964	chromosome X open reading frame 12
38368_at	down	0.048974	dUTP pyrophosphatase
33395_at	up	0.048977	DKFZP566C0424 protein
36432_at	up	0.049021	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)

36920_at	down	0.049082	myotubular myopathy 1
35830_at	up	0.049138	exportin 6
39531_at	up	0.049147	microtubule-associated protein 1B
31710_at	up	0.049156	
35550_at	down	0.04917	phosphate cytidyltransferase 1, choline, beta isoform
32643_at	up	0.049176	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV)
1213_at	down	0.049284	SFRS protein kinase 2
38765_at	down	0.049409	Dicer1, Dcr-1 homolog (Drosophila)
777_at	down	0.049529	GDP dissociation inhibitor 2
39854_r_at	up	0.049529	transport-secretion protein 2.2
36118_at	down	0.049576	nuclear receptor coactivator 1
39009_at	down	0.049585	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)
40106_at	up	0.049587	E1B-55kDa-associated protein 5
32597_at	down	0.049613	retinoblastoma-like 2 (p130)
37423_at	up	0.049689	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
32792_at	down	0.049898	GCIP-interacting protein p29
37900_at	down	0.049937	peroxisomal biogenesis factor 11B
218_at	down	0.050114	IK cytokine, down-regulator of HLA II
1983_at	up	0.050135	cyclin D2
38199_at	up	0.050157	similar to RIKEN cDNA 2610307I21
35370_at	down	0.050158	SPTF-associated factor 65 gamma
36509_at	down	0.050193	ribosomal protein L35a
41855_at	down	0.050238	histone acetyltransferase 1
33921_at	up	0.050257	glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1
32338_at	up	0.050322	DKFZP564C152 protein
31573_at	down	0.050336	ribosomal protein S25
35686_s_at	up	0.05038	mature T-cell proliferation 1
34508_r_at	up	0.050407	kinase phosphatase inhibitor 2
39264_at	up	0.050425	2'-5'-oligoadenylate synthetase 2, 69/71kDa
937_at	down	0.050456	
39507_at	down	0.050466	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
36460_at	down	0.05048	polymerase (RNA) I polypeptide C, 30kDa
1449_at	down	0.050486	proteasome (prosome, macropain) subunit, alpha type, 4
32982_at	down	0.050635	myelin transcription factor 2
41400_at	down	0.050664	thymidine kinase 1, soluble
41266_at	down	0.050685	integrin, alpha 6
336_at	up	0.050688	thromboxane A2 receptor
35083_at	up	0.050695	ferritin, light polypeptide
34563_at	up	0.050709	kinesin family member 14
39951_at	up	0.050726	plastin 1 (I isoform)

469_at	up	0.05075	ephrin-B3
1589_s_at	down	0.050778	interferon (alpha, beta and omega) receptor 2
32915_at	up	0.050787	
32319_at	up	0.050795	tumor necrosis factor (ligand) superfamily, member 4 (ta: transcriptionally activated glycoprotein 1, 34kDa)
40516_at	down	0.050823	aryl hydrocarbon receptor
40762_g_at	down	0.050837	solute carrier family 16 (monocarboxylic acid transporters), member 5
32872_at	up	0.050892	
32598_at	down	0.050917	NEL-like 2 (chicken)
40066_at	down	0.050921	ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)
37191_at	up	0.050937	phytanoyl-CoA hydroxylase interacting protein
36731_g_at	up	0.050945	ATP-binding cassette, sub-family C (CFTR/MRP), member 10
38032_at	up	0.050977	synaptic vesicle glycoprotein 2A
39891_at	down	0.051005	
40727_at	down	0.051151	anaphase-promoting complex subunit 10
34573_at	up	0.051166	ephrin-A3
37575_at	down	0.051171	
41837_at	up	0.051172	chromosome 14 open reading frame 132
39706_at	down	0.051192	copine III
39796_at	up	0.051208	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
37205_at	up	0.051225	F-box and leucine-rich repeat protein 7
33517_f_at	up	0.051227	melanoma antigen, family A, 3
37089_at	up	0.051376	a disintegrin and metalloproteinase domain 3a (cyritestir 1)
41525_at	up	0.051469	high-mobility group 20B
37387_r_at	down	0.05148	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1
41753_at	up	0.051513	actinin, alpha 4
40561_at	up	0.05152	T-cell leukemia, homeobox 2
33523_at	up	0.051666	alkaline phosphatase, intestinal
36041_at	up	0.051715	exonuclease 1
39789_at	up	0.051771	sarcolipin
36799_at	up	0.051797	frizzled homolog 2 (Drosophila)
41493_at	down	0.051813	ATPase, Class VI, type 11A
34820_at	up	0.051886	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)
36484_at	down	0.051889	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 3 (GalNAc-T3)
40381_at	up	0.051999	KIAA0972 protein
38230_at	up	0.052097	endothelial PAS domain protein 1
33961_at	up	0.052099	
40371_at	up	0.052175	dopamine receptor D2
36494_at	down	0.052182	spondyloepiphyseal dysplasia, late, pseudogene
33198_at	down	0.052191	binder of Arl Two

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35743_at	up	0.052209	cleavage and polyadenylation specific factor 4, 30kDa
34791_at	down	0.052211	t-complex 1
32811_at	up	0.05223	myosin IC
37381_g_at	down	0.052289	general transcription factor IIB
379_at	down	0.052302	ATP binding protein associated with cell differentiation
39519_at	down	0.052312	KIAA0692 protein
34167_s_at	up	0.052385	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7
31367_at	up	0.052421	KIAA0998 protein
36971_at	down	0.052422	likely ortholog of mouse Rw1
37021_at	down	0.052436	cathepsin H
37620_at	down	0.052482	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa
765_s_at	up	0.052582	lectin, galactoside-binding, soluble, 4 (galectin 4)
39003_at	down	0.052675	pituitary tumor-transforming 1 interacting protein
31962_at	up	0.052686	ribosomal protein L37a
551_at	down	0.052715	E1A binding protein p300
40491_at	up	0.052889	retinoblastoma binding protein 1-like 1
39692_at	down	0.052957	hypothetical protein DKFZp586F2423
32533_s_at	down	0.053017	vesicle-associated membrane protein 5 (myobrevin)
39064_at	down	0.053053	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)
35957_at	up	0.053064	stannin
36440_at	up	0.053117	pre T-cell antigen receptor alpha
39707_at	down	0.053118	myotubularin related protein 4
32335_r_at	down	0.053145	ubiquitin C
867_s_at	up	0.053202	thrombospondin 1
33545_at	up	0.053202	sodium channel, voltage-gated, type IV, alpha
716_at	up	0.053248	gamma-glutamyltransferase-like activity 1
37490_at	up	0.053251	solute carrier family 4, anion exchanger, member 3
34963_at	up	0.053255	collagen, type XIV, alpha 1 (undulin)
1878_g_at	down	0.053278	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
41218_at	down	0.053298	KIAA0570 gene product
37306_at	down	0.053313	cytoplasmic FMR1 interacting protein 1
32654_g_at	down	0.053395	bromodomain containing 8
1180_g_at	down	0.053406	
738_at	down	0.053443	5'-nucleotidase, cytosolic II
32843_s_at	up	0.05356	casein kinase 2, beta polypeptide
39818_at	down	0.053596	putative c-Myc-responsive
1984_s_at	up	0.05365	Rho GDP dissociation inhibitor (GDI) beta
34705_at	up	0.053743	similar to yeast BET3 (S. cerevisiae)



35147_at	up	0.053798	MCF.2 cell line derived transforming sequence-like solute carrier family 22 (organic anion transporter), member 6
36237_at	up	0.053829	
39070_at	down	0.053862	
39061_at	up	0.053904	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)
39457_r_at	up	0.053929	bone marrow stromal cell antigen 2
40466_at	up	0.053949	sorting nexin 4
38485_at	down	0.054018	nuclear transcription factor Y, gamma
37307_at	up	0.054022	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
633_s_at	up	0.054102	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2
883_s_at	up	0.054292	transcription factor Dp-2 (E2F dimerization partner 2)
815_at	up	0.054384	pim-1 oncogene
39549_at	down	0.054465	docking protein 1, 62kDa (downstream of tyrosine kinase 1)
35748_at	down	0.054501	neuronal PAS domain protein 2
32488_at	up	0.054503	eukaryotic translation elongation factor 1 beta 2
1125_s_at	up	0.054566	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)
38931_at	down	0.054596	CD44 antigen (homing function and Indian blood group system)
35047_at	up	0.054596	zinc finger protein, X-linked
36807_at	up	0.054671	regulatory factor X, 2 (influences HLA class II expression)
32745_at	down	0.054805	TED protein
33079_at	down	0.054837	mitochondrial ribosomal protein L40
38195_at	up	0.054849	syntaxin 6
40348_s_at	up	0.054929	KIAA0783 gene product
35675_at	up	0.055021	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
41655_at	up	0.055041	vinexin beta (SH3-containing adaptor molecule-1)
35502_at	up	0.055045	midline 2
39590_at	up	0.055058	anti-Mullerian hormone receptor, type II
39921_at	down	0.05506	amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)
1904_at	down	0.055112	cytochrome c oxidase subunit Vb
40326_at	up	0.055127	c-myc binding protein
39364_s_at	up	0.055204	cerebellin 1 precursor
32860_g_at	down	0.055251	protein phosphatase 1, regulatory (inhibitor) subunit 3C
39899_at	up	0.055292	signal transducer and activator of transcription 1, 91kDa
38850_at	up	0.055469	TSLC1-like 2
37725_at	down	0.055509	protein phosphatase 1, catalytic subunit, gamma isoform
32106_at	up	0.055553	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4
409_at	down	0.055578	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide

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33715_r_at	down	0.055635	general transcription factor IIH, polypeptide 2, 44kDa
32587_at	down	0.055636	zinc finger protein 36, C3H type-like 2
38172_at	down	0.055664	carbonyl reductase 3
37436_at	up	0.055701	mitochondrial capsule selenoprotein
41070_r_at	down	0.055707	transcription termination factor, mitochondrial
39841_at	down	0.055715	solute carrier family 16 (monocarboxylic acid transporters), member 6
35354_at	up	0.055782	synaptogyrin 1
38526_at	up	0.055797	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)
1412_g_at	up	0.055798	cytochrome P450, family 11, subfamily B, polypeptide 1
37840_at	up	0.055809	cyclic nucleotide gated channel alpha 1
36606_at	up	0.05594	carboxypeptidase E
36163_at	down	0.055944	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex)
34843_at	down	0.056006	KIAA0222 gene product
41418_at	up	0.056134	latrophilin 1
38416_at	down	0.056171	chaperonin containing TCP1, subunit 6A (zeta 1)
36998_s_at	down	0.056286	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)
34587_at	up	0.0563	eosinophil peroxidase
38627_at	up	0.056394	hepatic leukemia factor
1076_at	down	0.056444	interleukin 1, alpha
1337_s_at	up	0.056459	retinoic acid receptor, alpha
AFFX-BioDn-5_at	up	0.056496	
37694_at	down	0.056501	PHD finger protein 3
39337_at	down	0.056519	H2A histone family, member Z
37077_at	up	0.056579	pyruvate kinase, liver and RBC
38371_at	down	0.056601	proteasome (prosome, macropain) subunit, alpha type, 1
33205_at	up	0.056644	suppressor of Ty 3 homolog (S. cerevisiae)
33281_at	up	0.056699	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon
32303_at	up	0.05673	ets variant gene 3
32546_at	down	0.056793	fumarate hydratase
734_at	up	0.0568	
35022_at	up	0.056829	SRY (sex determining region Y)-box 5
32224_at	down	0.056859	KIAA0769 gene product
37001_at	down	0.056907	calpain 2, (m/II) large subunit
39991_at	up	0.056999	comeodesmosin
41496_at	up	0.057011	HCF-binding transcription factor Zhangfei
39894_f_at	down	0.057027	bromodomain containing 1
35824_at	down	0.057055	zinc finger protein 238

37499_at	up	0.057095	KIAA0408 gene product
36446_s_at	down	0.057135	hepatoma-derived growth factor (high-mobility group protein 1-like)
37994_at	down	0.057304	fragile X mental retardation 1
33670_at	up	0.057341	
41622_r_at	down	0.05735	zinc finger protein 266
41294_at	up	0.057454	keratin 7
39747_at	down	0.057465	polymerase (RNA) II (DNA directed) polypeptide G
2068_s_at	down	0.057538	E2F transcription factor 2
37751_at	down	0.057572	KIAA0255 gene product
33039_at	down	0.057696	T-cell receptor interacting molecule
1621_at	down	0.057779	CDC5 cell division cycle 5-like (S. pombe)
182_at	up	0.057817	inositol 1,4,5-triphosphate receptor, type 3
31587_at	up	0.057841	solute carrier family 14 (urea transporter), member 2
34402_at	down	0.057844	unr-interacting protein
36620_at	down	0.057858	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
39439_at	up	0.057864	
40738_at	up	0.057874	CD2 antigen (p50), sheep red blood cell receptor
36165_at	down	0.057904	cytochrome c oxidase subunit VIc
35267_g_at	down	0.057925	bladder cancer associated protein
41858_at	up	0.057932	FGF receptor activating protein 1
32013_at	down	0.057996	zinc finger protein 409
35958_at	up	0.058051	ADP-ribosylation factor-like 7
31851_at	down	0.058101	ret finger protein 2
33069_f_at	up	0.058119	UDP glycosyltransferase 2 family, polypeptide B15
32392_s_at	up	0.058127	UDP glycosyltransferase 1 family, polypeptide A4
39150_at	down	0.058159	ring finger protein 11
35831_at	up	0.058337	ATPase, Class II, type 9A
35434_at	up	0.058387	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)
39412_at	up	0.058422	tripartite motif-containing 26
39294_at	up	0.058457	nuclear receptor subfamily 2, group F, member 1
41638_at	down	0.058458	KIAA0073 protein
34404_at	down	0.05849	COP9 constitutive photomorphogenic homolog subunit 7, (Arabidopsis)
32733_at	down	0.05852	mitochondrial ribosomal protein S14
33706_at	up	0.058622	squamous cell carcinoma antigen recognised by T cells
40578_s_at	up	0.058655	tropomodulin 1
37165_f_at	up	0.058858	Rhesus blood group, CcEe antigens
35172_at	down	0.058889	tyrosylprotein sulfotransferase 2
AFFX-DapX-3_at	up	0.05895	

41705_at	up	0.059029	radical fringe homolog (Drosophila)
1735_g_at	up	0.059035	transforming growth factor, beta 3
36687_at	down	0.059039	cytochrome c oxidase subunit VIIb
33403_at	down	0.059201	DKFZP547E1010 protein
553_g_at	down	0.059352	Rho GTPase activating protein 1
31869_at	down	0.059449	SWAP-70 protein
715_s_at	up	0.059541	gamma-glutamyltransferase 1
40688_at	up	0.059541	linker for activation of T cells
33514_at	down	0.059565	calcium/calmodulin-dependent protein kinase IV
38019_at	up	0.059588	casein kinase 1, epsilon
36570_at	up	0.059666	calbindin 1, 28kDa
1680_at	up	0.059714	growth factor receptor-bound protein 7
2015_s_at	down	0.059737	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)
331_at	up	0.059749	
32117_at	up	0.059788	apoptosis antagonizing transcription factor
32606_at	down	0.059843	brain abundant, membrane attached signal protein 1
38256_s_at	down	0.059857	DKFZP564O092 protein
1657_at	up	0.059889	protein tyrosine phosphatase, receptor type, R
38414_at	down	0.060003	CDC20 cell division cycle 20 homolog (S. cerevisiae)
40710_at	up	0.060006	calmegin
36506_at	down	0.060098	A kinase (PRKA) anchor protein (yotiao) 9
36517_at	down	0.060144	U2(RNU2) small nuclear RNA auxiliary factor 1
38314_at	up	0.060166	capicua homolog (Drosophila)
38031_at	down	0.06017	KIAA0111 gene product
1915_s_at	up	0.060242	v-fos FBJ murine osteosarcoma viral oncogene homolog
1250_at	down	0.060379	protein kinase, DNA-activated, catalytic polypeptide
31309_r_at	up	0.060453	
31318_at	up	0.060492	
38183_at	down	0.060518	forkhead box F1
35953_at	up	0.060518	carboxypeptidase N, polypeptide 1, 50kD
40482_s_at	up	0.060522	transcriptional activator of the c-fos promoter
34073_s_at	up	0.060534	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1
499_at	up	0.060624	MAD1 mitotic arrest deficient-like 1 (yeast)
34096_at	up	0.060635	KIAA0912 protein
40453_s_at	down	0.060669	splicing factor, arginine/serine-rich 5
35554_f_at	up	0.060751	Zic family member 2 (odd-paired homolog, Drosophila)
38281_at	down	0.060874	caspase 7, apoptosis-related cysteine protease
41807_at	down	0.060901	sin3-associated polypeptide, 18kDa
35374_at	up	0.060921	rootletin
41506_at	down	0.060926	mitogen-activated protein kinase-activated protein kinase 5
32194_at	down	0.06103	CCAAT-box-binding transcription factor
386_g_at	up	0.0611	

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36572_r_at	down	0.06115	ADP-ribosylation factor-like 6 interacting protein
32965_f_at	up	0.061162	heat shock 70kDa protein 1B
34814_at	down	0.06127	SUMO-1 activating enzyme subunit 2
39399_at	up	0.061337	tubulin-specific chaperone d
38872_at	up	0.061352	zinc finger protein 230
31539_r_at	up	0.061358	
38483_at	up	0.061407	dullard homolog (Xenopus laevis)
838_s_at	up	0.061516	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)
41833_at	up	0.061566	jumping translocation breakpoint
33004_g_at	up	0.06165	NCK adaptor protein 2
39151_at	up	0.061669	astrotactin
33952_at	up	0.06176	zinc finger protein 306
35575_f_at	up	0.061928	zinc finger protein 253
40567_at	down	0.061963	tubulin, alpha 3
905_at	down	0.061983	guanylate kinase 1
39133_at	down	0.061983	GCN5 general control of amino-acid synthesis 5-like 1 (yeast)
41669_at	down	0.062016	KIAA0191 protein
39048_at	up	0.06202	Notch homolog 4 (Drosophila)
40134_at	down	0.062031	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex subunit f, isoform 2
610_at	down	0.062036	adrenergic, beta-2-, receptor, surface
445_at	up	0.062045	NK3 transcription factor related, locus 1 (Drosophila)
36353_at	up	0.062046	hairy and enhancer of split (Drosophila) homolog 2
40180_at	up	0.062046	insulin receptor substrate 2
32963_s_at	down	0.062118	Rag D protein
1458_at	up	0.062196	protein tyrosine phosphatase, non-receptor type 3
40667_at	up	0.062229	CD6 antigen
34821_at	down	0.062272	chromosome 6 open reading frame 80
38114_at	down	0.062321	RAD21 homolog (S. pombe)
40409_at	down	0.06235	aldehyde dehydrogenase 3 family, member A2
36900_at	up	0.062386	stromal interaction molecule 1
40604_at	down	0.062441	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
37608_g_at	up	0.062657	ketoheokinase (fructokinase)
38607_at	up	0.062688	transmembrane 4 superfamily member 5
31496_g_at	up	0.062707	chemokine (C motif) ligand 2
39005_s_at	down	0.062761	zinc finger protein 294
41038_at	down	0.062773	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)
731_f_at	up	0.062914	
776_at	down	0.062923	phosphatidylinositol glycan, class F

2050_s_at	down	0.06298	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
37892_at	up	0.062998	collagen, type XI, alpha 1
34237_at	down	0.063043	HBS1-like (S. cerevisiae)
AFFX-HUMGAPDH/M3 3197_M_at	up	0.063076	glyceraldehyde-3-phosphate dehydrogenase
41023_at	up	0.063109	complement component 8, alpha polypeptide
38408_at	up	0.063134	transmembrane 4 superfamily member 2
35552_at	up	0.063161	phosphate cytidyltransferase 1, choline, beta isoform
36058_at	up	0.063188	ASC-1 complex subunit P100
32592_at	up	0.063295	KIAA0323 protein
32559_s_at	down	0.063304	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)
31675_s_at	down	0.063337	phosphatase and tensin homolog (mutated in multiple advanced cancers 1), pseudogene 1
34003_at	down	0.063334	triosephosphate isomerase 1
34412_s_at	up	0.06344	peanut-like 1 (Drosophila)
37853_at	up	0.063455	urocortin
40125_at	down	0.063554	calnexin
36148_at	up	0.063582	amyloid beta (A4) precursor-like protein 1
35078_at	up	0.063583	intercellular adhesion molecule 4, Landsteiner-Wiener blood group
32967_at	up	0.06359	regulator of Fas-induced apoptosis
35939_s_at	up	0.063597	POU domain, class 4, transcription factor 1
40777_at	down	0.063706	catenin (cadherin-associated protein), beta 1, 88kDa
33448_at	up	0.063706	serine protease inhibitor, Kunitz type 1
36845_at	down	0.063755	nuclear matrix protein NXP2
33678_i_at	up	0.063774	tubulin, beta, 2
1956_s_at	up	0.063778	
34993_at	up	0.063791	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
39017_at	down	0.063812	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)
199_s_at	down	0.063818	protein kinase C-like 2
37779_at	up	0.063874	acid sphingomyelinase-like phosphodiesterase
522_s_at	up	0.063911	folate receptor 3 (gamma)
33822_at	up	0.063948	nuclear mitotic apparatus protein 1
34019_at	up	0.063949	cholinergic receptor, nicotinic, alpha polypeptide 3
1453_at	down	0.064036	MAD, mothers against decapentaplegic homolog 2 (Drosophila)
31733_at	up	0.064146	purinergic receptor P2X, ligand-gated ion channel, 3
38306_at	down	0.06416	brefeldin A-inhibited guanine nucleotide-exchange protein 1
36276_at	up	0.06418	contactin 2 (axonal)
851_s_at	up	0.064186	insulin receptor substrate 1

556_s_at	up	0.064191	glutathione S-transferase M4
35661_g_at	up	0.064238	S-antigen; retina and pineal gland (arrestin)
39339_at	up	0.064293	KIAA0792 gene product
36916_at	up	0.064357	sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase)
31559_at	up	0.064387	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2
35610_at	up	0.06442	matrilin 1, cartilage matrix protein
41145_at	down	0.064477	family with sequence similarity 13, member A1
41681_at	down	0.064546	ATP-binding cassette, sub-family B (MDR/TAP), member 7
32954_at	up	0.064582	DKFZP434D193 protein
32571_at	up	0.064689	methionine adenosyltransferase II, alpha
33684_at	up	0.064701	wingless-type MMTV integration site family, member 2B
38164_at	down	0.064739	retinitis pigmentosa GTPase regulator
32681_at	up	0.064752	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na <sup>+</sup> /H <sup>+</sup> , amiloride sensitive)
40623_at	down	0.064767	ubiquitin protein ligase
36763_at	up	0.064769	wingless-type MMTV integration site family, member 7A
40838_at	down	0.064777	zinc finger protein 292
40419_at	up	0.064956	stomatin
39195_s_at	up	0.064983	leucine-rich repeats and immunoglobulin-like domains 1
40506_s_at	down	0.065005	poly(A) binding protein, cytoplasmic 4 (inducible form)
38186_g_at	up	0.065027	paired box gene 2
32697_at	down	0.065062	inositol(myo)-1(or 4)-monophosphatase 1
35813_at	up	0.065103	transportin-SR
33895_at	down	0.065122	likely ortholog of mouse Sh3 domain YSC-like 1
40406_at	up	0.065199	macrophage stimulating, pseudogene 9
41162_at	up	0.065234	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
35368_at	down	0.06526	zinc finger protein 207
35019_at	up	0.065337	zinc finger protein 254
39460_g_at	up	0.065365	ribosomal protein S13
39647_s_at	up	0.065434	calcium channel, voltage-dependent, beta 2 subunit
31801_at	up	0.065498	
37081_at	up	0.065507	dynein, axonemal, heavy polypeptide 7
31765_at	up	0.065614	hypothetical protein FLJ20220
38668_at	down	0.065811	KIAA0553 protein
32050_r_at	down	0.065884	
35116_at	down	0.065906	KIAA0874 protein
36808_at	up	0.065972	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
40854_at	down	0.066118	ubiquinol-cytochrome c reductase core protein II

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35673_at	up	0.066212	Rho guanine nucleotide exchange factor (GEF) 5
40269_at	down	0.066219	PRP18 pre-mRNA processing factor 18 homolog (yeast)
1403_s_at	up	0.066241	chemokine (C-C motif) ligand 5
31436_s_at	up	0.066263	estrogen receptor 2 (ER beta)
308_f_at	up	0.066282	growth hormone 2
41476_at	up	0.066339	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
1195_s_at	down	0.066371	integrin cytoplasmic domain-associated protein 1
39096_at	down	0.066452	SON DNA binding protein
36945_at	up	0.066499	chromosome 12 open reading frame 8
39036_g_at	down	0.066538	progesterone induced protein
41029_at	up	0.066712	U1-snRNP binding protein homolog
35721_at	down	0.0668	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1
38949_at	up	0.066925	protein kinase C, theta
38945_at	up	0.067053	metal-regulatory transcription factor 1
34626_at	up	0.06707	hypermethylated in cancer 1
744_at	down	0.067118	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase)
34596_at	up	0.067122	casein kappa
36935_at	down	0.067265	RAS p21 protein activator (GTPase activating protein) 1
1952_s_at	down	0.067351	MAD, mothers against decapentaplegic homolog 5 (Drosophila)
41278_at	down	0.067459	BAF53
643_at	up	0.067476	nuclear receptor subfamily 0, group B, member 2
1399_at	down	0.067506	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)
32545_r_at	up	0.067532	Ras suppressor protein 1
34649_at	down	0.067605	decorin
37966_at	up	0.06761	parvin, beta
40832_s_at	down	0.067654	lamina-associated polypeptide 1B
38672_at	up	0.067756	protein phosphatase 1, regulatory subunit 10
35576_f_at	up	0.067819	histone 1, H2bl
33438_at	up	0.067968	WW domain binding protein 2
35481_at	up	0.068025	myosin heavy chain Myr 8
32217_at	down	0.068042	chromosome 12 open reading frame 22
228_at	down	0.068127	v-rat simian leukemia viral oncogene homolog B (ras related; GTP binding protein)
464_s_at	down	0.06822	interferon-induced protein 35
39552_at	down	0.068223	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
41110_at	down	0.068425	cullin 5
37023_at	down	0.068458	lymphocyte cytosolic protein 1 (L-plastin)



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36948_at	down	0.068499	CREBBP/EP300 inhibitory protein 1
40963_at	up	0.068522	ATP-binding cassette, sub-family A (ABC1), member 4
38633_at	down	0.068526	metastasis associated 1
31339_at	up	0.068694	protease inhibitor 15
AFFX-CreX-5_st	up	0.068736	
41051_at	down	0.068762	translin-associated factor X
33842_at	up	0.06881	hypothetical protein FLJ11560
36597_at	down	0.068981	nucleolar and coiled-body phosphoprotein 1
31523_f_at	up	0.068994	histone 1, H2be
41460_at	down	0.069064	RNA binding motif protein 14
36958_at	up	0.069077	zyxin
36483_at	down	0.069179	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase 3 (GalNAc-T3)
32274_r_at	up	0.069303	
36616_at	down	0.069311	DAZ associated protein 2
39721_at	up	0.069372	ephrin-B1
950_at	down	0.06943	translocation protein 1
33354_at	down	0.069464	E3 ubiquitin ligase SMURF2
40571_at	down	0.0695	myosin VA (heavy polypeptide 12, myosin)
41343_at	down	0.06951	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2
38159_at	up	0.069545	
33989_f_at	up	0.069619	testis enhanced gene transcript (BAX inhibitor 1)
39646_at	up	0.06966	calcium channel, voltage-dependent, beta 2 subunit
39141_at	up	0.069763	ATP-binding cassette, sub-family F (GCN20), member 1
966_at	up	0.069776	RAD54-like (S. cerevisiae)
40660_at	up	0.069809	nuclear receptor subfamily 4, group A, member 3
35037_at	up	0.069895	solute carrier family 28 (sodium-coupled nucleoside transporter), member 1
36978_at	down	0.069901	proteasome (prosome, macropain) activator subunit 4
1446_at	down	0.069924	proteasome (prosome, macropain) subunit, alpha type, 2
41296_s_at	down	0.069939	START domain containing 7
36104_at	down	0.06998	ubiquinol-cytochrome c reductase hinge protein
238_at	down	0.07003	ribosomal protein S6 kinase, 70kDa, polypeptide 1
36667_at	up	0.070033	phosphorylase, glycogen; brain
39992_at	up	0.070076	solute carrier family 22 (organic cation transporter), member 1-like
35864_at	up	0.070114	acrosin
39295_s_at	up	0.070249	Arg/Abl-interacting protein ArgBP2
38522_s_at	down	0.070415	CD22 antigen
40916_at	down	0.070458	hypothetical protein FLJ10097

37230_at	down	0.070461	KIAA0469 gene product
39717_g_at	down	0.07051	mitochondrial ribosomal protein L33
35793_at	down	0.07062	Ras-GTPase activating protein SH3 domain-binding protein 2
39633_at	up	0.070855	S100 calcium binding protein A3
35923_at	up	0.070865	cholecystokinin B receptor
32615_at	down	0.070887	aspartyl-tRNA synthetase
40761_at	down	0.071214	solute carrier family 16 (monocarboxylic acid transporters), member 5
32108_at	up	0.071219	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)
38392_at	down	0.071227	actin related protein 2/3 complex, subunit 5, 16kDa
35275_at	up	0.071315	adaptor-related protein complex 1, gamma 1 subunit
AFFX-hum_alu_at	up	0.07143	
35527_at	up	0.071458	calcium channel, voltage-dependent, alpha 2/delta subunit 1
34752_at	down	0.071628	NIMA (never in mitosis gene a)-related kinase 7
35634_at	down	0.071647	mitogen-activated protein kinase kinase kinase 7 interacting protein 1
36452_at	up	0.071789	synaptopodin
35975_at	down	0.071826	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3
33707_at	up	0.071894	phospholipase A2, group IVC (cytosolic, calcium-independent)
34274_at	down	0.071954	RNA binding motif protein 16
40282_s_at	up	0.071967	D component of complement (adipsin)
40929_at	down	0.072007	SOCS box-containing WD protein SWIP-1
37024_at	down	0.072145	lipopolysaccharide-induced TNF factor
1005_at	up	0.072186	dual specificity phosphatase 1
38968_at	up	0.072257	SH3-domain binding protein 5 (BTK-associated)
34013_f_at	up	0.072278	POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1)
33867_s_at	down	0.072333	RNA binding motif, single stranded interacting protein 1
38096_f_at	down	0.072339	major histocompatibility complex, class II, DP beta 1
37657_at	up	0.072576	paralemmin
33388_at	up	0.072624	testis expressed gene 261
39561_at	up	0.072667	chromobox homolog 6
34578_at	up	0.072676	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)
40458_at	down	0.072706	signal transducer and activator of transcription 5A
934_at	up	0.072711	glycosylphosphatidylinositol specific phospholipase D1
36875_at	down	0.072713	inhibitor of Bruton's tyrosine kinase
35526_at	up	0.07279	complement component 9
38359_at	up	0.072822	RAS guanyl releasing protein 2 (calcium and DAG-regulated)

41156_g_at	down	0.072839	catenin (cadherin-associated protein), alpha 1, 102kDa
37000_at	down	0.072839	DKFZP564B167 protein
450_g_at	down	0.072846	cell growth regulatory with ring finger domain
38892_at	down	0.072861	KIAA0240 protein
33224_at	up	0.072965	cysteine and histidine rich 1
33646_g_at	up	0.073003	GM2 ganglioside activator protein
31667_r_at	up	0.073068	nuclear receptor subfamily 2, group E, member 3
32853_at	down	0.073154	translocase of outer mitochondrial membrane 70 homolog A (yeast)
34193_at	up	0.073157	cell adhesion molecule with homology to L1CAM (close homolog of L1)
36017_at	up	0.073176	chromosome 13 open reading frame 1
36110_at	down	0.073203	RAB5A, member RAS oncogene family
37861_at	up	0.073269	CD1E antigen, e polypeptide
41826_at	up	0.073366	KIAA1467 protein
31682_s_at	up	0.073398	chondroitin sulfate proteoglycan 2 (versican)
34389_at	up	0.073463	collagen, type XIV, alpha 1 (undulin)
33627_at	up	0.073511	phosphoinositide-3-kinase, catalytic, delta polypeptide
37238_s_at	up	0.07355	membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase
39167_r_at	down	0.073633	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1
38735_at	up	0.073757	KIAA0513 gene product
38477_at	down	0.073758	diphtheria toxin resistance protein required for diphthamid biosynthesis-like 1 (S. cerevisiae)
36399_at	up	0.073791	pre-mRNA splicing SR protein rA4
40150_at	down	0.074001	small nuclear ribonucleoprotein D3 polypeptide 18kDa
40276_at	down	0.074021	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)
31948_at	down	0.07403	ribosomal protein S21
34269_at	down	0.074059	erythroid differentiation-related factor 1
1568_s_at	down	0.074061	interferon (alpha, beta and omega) receptor 2
33242_at	down	0.074072	hypothetical protein DT1P1A10
31967_at	up	0.074076	nephrosis 1, congenital, Finnish type (nephrin)
40167_s_at	down	0.074152	likely ortholog of mouse WD-40-repeat-containing protein with a SOCS box 2
35766_at	down	0.074163	keratin 18
41553_at	up	0.074209	chromosome 8 open reading frame 1
755_at	down	0.07422	inositol 1,4,5-triphosphate receptor, type 1
34697_at	up	0.074223	low density lipoprotein receptor-related protein 6
38271_at	down	0.074257	histone deacetylase 4
32629_f_at	up	0.074409	butyrophilin, subfamily 3, member A1
40263_at	up	0.074575	zinc finger protein-like 1

34357_g_at	down	0.074581	SRB7 suppressor of RNA polymerase B homolog (yeast)
AFFX-BioB-M_at	up	0.074593	
36507_at	up	0.074761	zinc finger protein 282
37377_i_at	up	0.074824	lamin A/C
39381_at	down	0.074885	PHD finger protein 10
38374_at	down	0.074924	TGFB inducible early growth response
32961_at	down	0.075047	c-myc promoter-binding protein
38219_at	down	0.075065	v-crk sarcoma virus CT10 oncogene homolog (avian)
40517_at	down	0.075102	KIAA0372 gene product
40825_at	up	0.075117	microtubule-associated protein, RP/EB family, member 3
35208_at	down	0.075192	KIAA0874 protein
37521_s_at	down	0.075228	nucleolar cysteine-rich protein
37173_at	up	0.07526	centromere protein E, 312kDa
31738_at	up	0.075288	
38071_at	down	0.075384	heterogeneous nuclear ribonucleoprotein F
33285_i_at	down	0.075391	hypothetical protein FLJ21168
153_f_at	up	0.075466	histone 1, H2bj
32734_at	down	0.075516	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform
39360_at	down	0.07553	sorting nexin 3
39509_at	down	0.07559	programmed cell death 4 (neoplastic transformation inhibitor)
39852_at	down	0.075598	spastic paraplegia 20, spartin (Troyer syndrome)
32333_at	up	0.075602	
36535_at	down	0.075653	microfibrillar-associated protein 1
39780_at	down	0.075735	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
35488_at	down	0.075738	small nuclear RNA activating complex, polypeptide 1, 43kDa
545_g_at	down	0.075781	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
41711_at	up	0.075904	thioredoxin reductase 2
34613_at	up	0.075912	KIAA1086 protein
33831_at	down	0.07592	CREB binding protein (Rubinstein-Taybi syndrome)
31797_at	down	0.075936	TBP-like 1
34548_at	up	0.075953	cytochrome P450, family 11, subfamily B, polypeptide 1
37030_at	down	0.076042	expressed in T-cells and eosinophils in atopic dermatitis
845_at	up	0.076077	signal transducer and activator of transcription 6, interleukin-4 induced
39253_s_at	down	0.076112	v-ras simian leukemia viral oncogene homolog A (ras related)
1821_at	down	0.076123	

41777_at	down	0.07617	ATPase, H <sup>+</sup> transporting, lysosomal interacting protein 2
34457_at	up	0.076243	solute carrier family 30 (zinc transporter), member 3
41061_at	down	0.076272	huntingtin interacting protein 1
34829_at	up	0.076322	dyskeratosis congenita 1, dyskerin
35751_at	down	0.076335	succinate dehydrogenase complex, subunit B, iron sulfur (lp)
35396_at	up	0.076518	hyaluronan synthase 2
39420_at	down	0.076789	DNA-damage-inducible transcript 3
100_g_at	up	0.076854	Rab geranylgeranyltransferase, alpha subunit
33863_at	up	0.076937	hypoxia up-regulated 1
36980_at	down	0.076989	proline rich 2
41736_g_at	up	0.077002	KIAA0870 protein
40148_at	down	0.077005	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)
36216_at	down	0.077027	sorting nexin 4
33656_at	down	0.077078	ribosomal protein L37
135_g_at	down	0.077114	abl-interactor 2
41512_at	down	0.077118	BRCA1 associated protein
1451_s_at	up	0.07736	osteoblast specific factor 2 (fasciclin I-like)
36224_g_at	down	0.077412	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
31903_at	up	0.077415	synovial sarcoma translocation gene on chromosome:18 like 1
33632_g_at	down	0.077589	similar to S. pombe dim1+
40625_f_at	up	0.07767	metaxin 1
37541_at	up	0.077734	selectin P ligand
692_s_at	up	0.077795	superoxide dismutase 3, extracellular
34259_at	up	0.07782	KIAA0664 protein
32871_at	up	0.077851	
41806_at	up	0.077878	fibroblast growth factor 2 (basic)
40961_at	down	0.077885	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
35671_at	up	0.077932	general transcription factor IIIC, polypeptide 1, alpha 220kDa
40379_at	up	0.077985	cytochrome P450, family 2, subfamily E, polypeptide 1
37163_at	down	0.077986	DKFZP586C1619 protein
33619_at	down	0.078048	ribosomal protein S13
424_s_at	up	0.07813	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
31758_at	up	0.07818	
38779_r_at	up	0.078277	hepatoma-derived growth factor (high-mobility group protein 1-like)
38102_at	down	0.078302	hypothetical protein FLJ34588
32768_at	up	0.078331	tudor domain containing 3
33659_at	up	0.078352	cofilin 1 (non-muscle)

36374_at	up	0.078482	
38006_at	down	0.078527	CD48 antigen (B-cell membrane protein)
38927_i_at	up	0.078558	tyrosinase (oculocutaneous albinism IA)
36094_at	up	0.078582	troponin T3, skeletal, fast
350_at	down	0.078582	zinc finger protein 161
33155_at	up	0.078626	iduronidase, alpha-L-
39315_at	up	0.078642	angiopoietin 1
33162_at	down	0.078765	insulin receptor
1440_s_at	down	0.078833	tumor necrosis factor receptor superfamily, member 6
37566_at	up	0.078937	KIAA1045 protein
40467_at	down	0.079211	succinate dehydrogenase complex, subunit D, integral membrane protein
211_at	down	0.079258	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
36282_at	up	0.079286	
39427_at	down	0.079371	ubiquinol-cytochrome c reductase binding protein
39810_at	down	0.079388	hypothetical protein MGC2749
41824_at	down	0.079408	CGI-48 protein
41508_at	up	0.079432	early growth response 4
1614_s_at	down	0.079473	ubiquitin specific protease 6 (Tre-2 oncogene)
1072_g_at	up	0.079479	GATA binding protein 2
36582_g_at	down	0.079698	glycyl-tRNA synthetase
35105_at	up	0.079724	sciellin
34598_at	up	0.079789	tenascin R (restrictin, janusin)
35154_at	up	0.079876	BTB (POZ) domain containing 2
40290_f_at	down	0.080058	sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase)
34201_at	down	0.080202	DnaJ (Hsp40) homolog, subfamily A, member 2
40870_g_at	down	0.08021	RNA binding motif protein 6
36610_at	down	0.080302	R3H domain (binds single-stranded nucleic acids) containing
36155_at	up	0.080485	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2
33209_at	down	0.080629	YY1 transcription factor
40887_g_at	up	0.080665	eukaryotic translation elongation factor 1 alpha 1
617_at	down	0.080689	acid phosphatase, prostate
35214_at	up	0.080736	UDP-glucose dehydrogenase
916_at	up	0.080801	protein tyrosine phosphatase, receptor type, N
40279_at	up	0.080847	KIAA0121 gene product
38712_at	down	0.080849	chromosome 1 open reading frame 9
41120_at	up	0.080863	aminomethyltransferase (glycine cleavage system prote T)
37813_at	up	0.08087	
1486_at	up	0.080961	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa

34351_at	up	0.081014	phospholipase C, gamma 1 (formerly subtype 148)
34809_at	down	0.081037	KIAA0999 protein
39040_at	down	0.081117	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
40689_at	down	0.081186	sel-1 suppressor of lin-12-like (C. elegans)
931_at	down	0.081247	Epstein-Barr virus induced gene 2 (lymphocyte-specific C protein-coupled receptor)
39147_g_at	up	0.081251	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
38116_at	down	0.08134	KIAA0101 gene product
1682_s_at	up	0.081428	ATP-binding cassette, sub-family B (MDR/TAP), member 1
36519_at	down	0.081516	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
40294_at	up	0.081521	ATP-binding cassette, sub-family B (MDR/TAP), member 9
38567_at	down	0.081526	CD1D antigen, d polypeptide
160029_at	down	0.081576	protein kinase C, beta 1
195_s_at	down	0.081607	caspase 4, apoptosis-related cysteine protease
36748_at	up	0.081853	synapsin II
475_at	up	0.081884	receptor (TNFRSF)-interacting serine-threonine kinase 1
31423_at	up	0.081988	
35907_at	up	0.081994	cyclin F
39033_at	down	0.082005	chromosome 1 open reading frame 8
31734_at	up	0.082019	homeo box C11
32640_at	up	0.082173	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor
39498_at	up	0.082268	FXYD domain containing ion transport regulator 2
1253_at	down	0.082282	glycogen synthase kinase 3 beta
33435_r_at	down	0.082325	BET1 homolog (S. cerevisiae)
35810_at	down	0.082362	actin related protein 2/3 complex, subunit 3, 21kDa
33964_at	up	0.082441	crystallin, gamma C
40866_at	down	0.082452	nipsnap homolog 1 (C. elegans)
37045_at	down	0.082479	sorting nexin 19
39431_at	down	0.082604	aminopeptidase puromycin sensitive
38514_at	down	0.082742	immunoglobulin lambda-like polypeptide 1
33876_at	up	0.082748	transcriptional co-activator with PDZ-binding motif (TAZ)
882_at	up	0.082785	
34123_at	up	0.082836	colony stimulating factor 1 (macrophage)
34533_at	up	0.082873	
33543_s_at	down	0.082933	hypothetical protein FLJ32746
			pinin, desmosome associated protein
37980_at	down	0.082971	CBF1 interacting corepressor
574_s_at	down	0.083007	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
789_at	up	0.083148	early growth response 1

34163_g_at	down	0.083192	RNA binding protein with multiple splicing
39718_r_at	down	0.083273	mitochondrial ribosomal protein L33
1136_at	down	0.083343	deoxythymidylate kinase (thymidylate kinase)
33893_r_at	down	0.08337	KARP-1-binding protein
40673_at	up	0.083476	acyl-Coenzyme A dehydrogenase, short/branched chain
36872_at	down	0.08356	cyclic AMP phosphoprotein, 19 kD
31930_f_at	up	0.083573	Rhesus blood group, CcEe antigens
40119_at	down	0.083591	cartilage associated protein
241_g_at	up	0.083623	spermidine synthase
519_g_at	up	0.083723	nuclear receptor subfamily 1, group H, member 2
37827_r_at	down	0.083832	chromosome 21 open reading frame 5
37679_at	down	0.083856	interferon-related developmental regulator 1
37385_at	down	0.08386	peptidyl-prolyl isomerase G (cyclophilin G)
33760_at	down	0.083864	peroxisomal biogenesis factor 14
671_at	up	0.083879	secreted protein, acidic, cysteine-rich (osteonectin)
35143_at	down	0.083893	hypothetical protein DKFZp566A1524
35946_at	up	0.083985	NEL-like 1 (chicken)
34678_at	down	0.084027	fer-1-like 3, myoferlin (C. elegans)
36121_at	up	0.084131	epsin 2
35413_s_at	up	0.084141	zinc finger protein 22 (KOX 15)
41197_at	down	0.084209	RAD23 homolog A (S. cerevisiae)
32173_at	up	0.084294	translational inhibitor protein p14.5
39791_at	down	0.084465	ATPase, Ca++ transporting, cardiac muscle, slow twitch
41124_r_at	down	0.084468	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)
41573_at	down	0.08456	Sp3 transcription factor
31805_at	up	0.084593	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
33080_s_at	up	0.084607	RAP1, GTPase activating protein 1
109_at	down	0.084611	Rab9 effector p40
34270_at	up	0.084688	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
37406_at	down	0.084705	microtubule-associated protein, RP/EB family, member 2
664_at	down	0.08478	interleukin 8 receptor, beta
36350_at	up	0.084859	
32883_at	down	0.084885	KRAB zinc finger protein KR18
35901_at	up	0.08489	plwi-like 1 (Drosophila)
1885_at	up	0.084893	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)
40701_at	up	0.085053	ubiquitin specific protease 13 (isopeptidase T-3)



268_at	down	0.085065	platelet/endothelial cell adhesion molecule (CD31 antigen)
1845_at	down	0.085084	mitogen-activated protein kinase kinase 4
41813_at	up	0.085175	nucleoporin 210
37282_at	down	0.085322	MAD2 mitotic arrest deficient-like 1 (yeast)
39883_at	down	0.085337	putative dimethyladenosine transferase
39581_at	down	0.085337	cystatin A (stefin A)
40558_at	up	0.085339	guanylate cyclase activator 1B (retina)
1143_s_at	down	0.085382	
37796_at	up	0.085405	leucine rich repeat neuronal 4
40758_at	down	0.085415	immature colon carcinoma transcript 1
AFFX-M27830_3_at	up	0.0855	
36462_at	up	0.085538	SMYD family member 5
31853_at	down	0.08559	embryonic ectoderm development
37293_at	down	0.085666	KIAA0097 gene product
38705_at	down	0.085669	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)
37588_s_at	up	0.085678	mitogen-activated protein kinase 8 interacting protein 2
40211_at	down	0.08573	heterogeneous nuclear ribonucleoprotein A1
467_at	down	0.08595	osteoclast stimulating factor 1
38530_at	up	0.086109	hypothetical protein FLJ22709
40048_at	down	0.086249	pumilio homolog 1 (Drosophila)
34223_at	up	0.086252	colony stimulating factor 3 receptor (granulocyte)
33240_at	up	0.0863	likely ortholog of mouse semaF cytoplasmic domain associated protein 3
33886_at	down	0.086302	spectrin SH3 domain binding protein 1
39832_at	up	0.086357	arsenate resistance protein ARS2
31638_at	up	0.086423	
41814_at	down	0.086559	fucosidase, alpha-L- 1, tissue
31800_at	up	0.086561	
31979_at	up	0.086615	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
34961_at	up	0.086616	T cell activation, increased late expression
35597_at	up	0.086723	phosphoprotein regulated by mitogenic pathways
33529_at	up	0.086755	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
38889_at	up	0.086863	MAD, mothers against decapentaplegic homolog (Drosophila) interacting protein, receptor activation anc
39221_at	down	0.086888	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2
32443_at	up	0.087	zinc finger protein 157 (HZF22)
34011_at	up	0.08701	harakiri, BCL2 interacting protein (contains only BH3 domain)
39643_at	up	0.087011	polymerase (DNA directed), gamma 2, accessory subunit
37935_at	up	0.08708	PRP4 pre-mRNA processing factor 4 homolog (yeast)

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39749_at	down	0.087136	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
36865_at	down	0.08718	KIAA0759 protein
36081_s_at	down	0.087181	chromosome 21 open reading frame 18
38347_at	down	0.087211	elongation protein 4 homolog (S. cerevisiae)
485_at	up	0.087219	
1001_at	up	0.087263	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains
35293_at	down	0.087479	Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro)
40733_f_at	up	0.087601	msh homeo box homolog 2 (Drosophila)
34474_at	down	0.087639	
41420_at	down	0.087753	insulin-like growth factor binding protein 5
210_at	up	0.08778	phospholipase C, beta 2
40901_at	down	0.087859	striatin, calmodulin binding protein 3
34708_at	up	0.087884	ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)
1671_s_at	up	0.087925	mitogen-activated protein kinase 14
33165_at	down	0.087974	target of EGR1, member 1 (nuclear)
31679_at	up	0.087997	
39290_f_at	up	0.088024	PAI-1 mRNA-binding protein
40480_s_at	down	0.088156	FYN oncogene related to SRC, FGR, YES
953_g_at	down	0.088165	
35845_at	down	0.088184	SEC24 related gene family, member B (S. cerevisiae)
41125_r_at	up	0.088253	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)
32190_at	down	0.088305	fatty acid desaturase 2
41117_s_at	up	0.088317	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 2
39824_at	up	0.088333	protein tyrosine phosphatase type IVA, member 3
38237_at	up	0.088414	gamma-glutamyltransferase-like activity 1
31713_s_at	up	0.088448	discs, large (Drosophila) homolog-associated protein 2
37323_r_at	up	0.088637	hydroxyprostaglandin dehydrogenase 15-(NAD)
39862_at	up	0.088689	KIAA0296 gene product
31594_at	up	0.088804	keratin, hair, acidic, 3A
33272_at	up	0.088835	serum amyloid A1
38907_at	up	0.088895	
32927_at	down	0.088975	
41425_at	down	0.089008	Friend leukemia virus integration 1
39396_at	down	0.089017	lysophospholipase I
34858_at	up	0.089029	potassium channel tetramerisation domain containing 2
32067_at	up	0.089124	cAMP responsive element modulator
35473_at	up	0.08921	collagen, type I, alpha 1

38073_at	down	0.089213	RNA (guanine-7-) methyltransferase
34859_at	up	0.089268	melanoma antigen, family D, 2
38048_at	up	0.089393	RNA binding protein with multiple splicing
38061_at	up	0.08946	ribosomal protein S16
34671_at	down	0.08955	polymerase (RNA) III (DNA directed) (62kD)
32813_s_at	up	0.089623	katanin p80 (WD repeat containing) subunit B 1
39829_at	up	0.089659	ADP-ribosylation factor-like 7
34736_at	up	0.089693	cyclin B1
40515_at	down	0.08972	eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
37763_at	up	0.089731	retinoid X receptor, beta
33984_at	up	0.089752	heat shock 90kDa protein 1, beta
32025_at	down	0.089771	transcription factor 7-like 2 (T-cell specific, HMG-box)
38990_at	down	0.089788	F-box only protein 9
38117_at	up	0.089832	SEC24 related gene family, member C (S. cerevisiae)
36784_at	down	0.090005	chorionic somatomammotropin hormone-like 1
32662_at	up	0.090014	mediator of DNA damage checkpoint 1
41535_at	down	0.090077	CDK2-associated protein 1
39152_f_at	down	0.0901	coilin
2069_s_at	down	0.090137	catenin (cadherin-associated protein), alpha 1, 102kDa
35307_at	down	0.090206	GDP dissociation inhibitor 2
35783_at	down	0.090268	vesicle-associated membrane protein 3 (cellubrevin)
909_g_at	down	0.090304	interferon-induced protein with tetratricopeptide repeats :
34038_at	up	0.090364	solute carrier family 6 (neurotransmitter transporter, GABA), member 13
37723_at	down	0.090364	cyclin G2
39913_at	up	0.090436	heparan sulfate 6-O-sulfotransferase 1
36511_at	down	0.09055	SAC1 suppressor of actin mutations 1-like (yeast)
31846_at	up	0.090573	ras homolog gene family, member D
38419_at	down	0.090574	KIAA0196 gene product
1745_at	down	0.090606	
34680_s_at	down	0.090628	KIAA0107 gene product
31833_at	up	0.090658	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha
39385_at	up	0.090659	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)
37768_at	up	0.0908	N-methylpurine-DNA glycosylase
34161_at	up	0.090915	lactoperoxidase
41868_at	up	0.090976	gamma-glutamyltransferase 1
37940_f_at	up	0.090998	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C
35230_at	up	0.091025	TIR domain containing adaptor inducing interferon-beta
40107_at	up	0.091064	aldolase C, fructose-bisphosphate

40764_at	up	0.091092	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
37685_at	down	0.091314	phosphatidylinositol binding clathrin assembly protein
1288_s_at	up	0.091336	eukaryotic translation elongation factor 1 alpha 1
33379_at	up	0.09136	synovial sarcoma, X breakpoint 2 interacting protein
39641_at	up	0.091498	uracil-DNA glycosylase 2
38739_at	down	0.091509	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
35807_at	up	0.091617	cytochrome b-245, alpha polypeptide
36213_at	up	0.09167	malignant fibrous histiocytoma amplified sequence 1
31522_f_at	up	0.091671	histone 1, H2bf
36184_at	up	0.091691	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI)
806_at	up	0.091752	cytokine-inducible kinase
2081_s_at	down	0.091827	protein kinase C, theta
37621_at	down	0.091829	interleukin 6 signal transducer (gp130, oncostatin M receptor)
41334_r_at	down	0.091888	
36613_at	up	0.092021	interferon-related developmental regulator 2
32878_f_at	down	0.09204	
34908_at	up	0.092066	hypothetical protein FLJ13946
37212_at	up	0.0921	Sp2 transcription factor
2084_s_at	up	0.092203	ets variant gene 4 (E1A enhancer binding protein, E1AF)
32856_at	up	0.092236	KIAA0819 protein
39219_at	down	0.092383	CCAAT/enhancer binding protein (C/EBP), gamma
37053_at	up	0.092455	ATPase, Ca++ transporting, plasma membrane 2
38962_at	up	0.092537	KIAA0298 gene product
36624_at	up	0.092613	IMP (inosine monophosphate) dehydrogenase 2
40757_at	up	0.092646	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
31780_f_at	up	0.092646	
37438_at	up	0.092667	KIAA0419 gene product
35844_at	up	0.092675	syndecan 4 (amphiglycan, ryudocan)
AFFX-BioB-M_st	up	0.092696	
38695_at	down	0.092773	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
31446_s_at	up	0.092903	proline rich 5 (salivary)
32747_at	down	0.092991	aldehyde dehydrogenase 2 family (mitochondrial)
32129_at	down	0.093034	zinc finger protein 364
37998_at	up	0.093081	superkiller viralicidic activity 2-like (S. cerevisiae)

40944_at	down	0.09309	TGFB inducible early growth response 2
31512_at	up	0.093117	immunoglobulin kappa variable 1-13
41268_g_at	down	0.093129	KIAA1049 protein
31960_f_at	up	0.093132	G antigen 2
2009_at	up	0.093184	PTK2B protein tyrosine kinase 2 beta
37520_at	down	0.093259	nucleolar cysteine-rich protein
32300_s_at	up	0.09328	tyrosine hydroxylase
36837_at	up	0.093336	kinesin family member 2C
39834_at	up	0.093358	cholinergic receptor, nicotinic, epsilon polypeptide
40465_at	down	0.09338	prp28, U5 snRNP 100 kd protein
33965_at	up	0.093408	chemokine (C-C motif) ligand 1
41068_at	down	0.09347	outer dense fiber of sperm tails 2
35100_at	up	0.093484	sialyltransferase 8C (alpha2,3Galbeta1,4GlcNAcalpha 2,8-sialyltransferase)
38171_at	up	0.093582	WD-repeat protein
34101_at	up	0.093618	
35279_at	down	0.09364	Tax1 (human T-cell leukemia virus type I) binding protein 1
34129_at	up	0.093741	tomosyn-like
38081_at	down	0.093785	leukotriene A4 hydrolase
33923_s_at	down	0.09381	PR domain containing 2, with ZNF domain
39965_at	up	0.093868	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)
40691_at	down	0.093908	zinc finger protein 274
35562_at	up	0.093917	histone 1, H2bj
40853_at	down	0.093992	ATPase, Class V, type 10D
34112_r_at	up	0.094039	
1073_at	down	0.094039	transcription elongation factor A (SII), 1
37535_at	down	0.094144	cAMP responsive element binding protein 1
32140_at	up	0.094211	sortilin-related receptor, L(DLR class) A repeats-containing
33077_at	up	0.094215	
34028_at	down	0.094218	G protein-coupled receptor 19
35356_at	down	0.094405	hypothetical protein MGC9651
40797_at	down	0.094519	a disintegrin and metalloproteinase domain 10
38569_at	up	0.094591	nuclear respiratory factor 1
1715_at	down	0.094642	tumor necrosis factor (ligand) superfamily, member 10
36277_at	up	0.094818	CD3E antigen, epsilon polypeptide (TiT3 complex)
34529_at	up	0.094849	
35445_at	up	0.0949	sorting nexin 26
32879_at	down	0.094954	
41635_at	down	0.094971	Wilms tumor 1 associated protein
38673_s_at	down	0.094985	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
37118_at	up	0.095049	ret finger protein-like 1 antisense

35306_at	down	0.095212	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15
40992_s_at	down	0.09541	sin3-associated polypeptide, 30kDa
37891_at	up	0.095425	
39448_r_at	up	0.095584	B7 gene
38843_at	down	0.095688	high-mobility group protein 2-like 1
39224_at	down	0.0957	centaurin, delta 1
39143_at	down	0.095718	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
39985_r_at	up	0.095724	FKBP-associated protein
38592_s_at	up	0.095754	KIAA0284 protein
1518_at	up	0.095784	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
35605_at	up	0.095808	angiopoietin-like factor
41712_at	down	0.095851	likely ortholog of mouse aquarius
35999_r_at	down	0.095865	KIAA0781 protein
36735_f_at	up	0.09588	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2
33710_at	down	0.095883	putative protein similar to nessy (Drosophila)
32888_at	up	0.095889	leukocyte tyrosine kinase
37397_at	down	0.095893	platelet/endothelial cell adhesion molecule (CD31 antigen)
41528_at	up	0.095958	
40766_at	up	0.096077	complement component 4A
36389_at	down	0.096078	class-I MHC-restricted T cell associated molecule
39666_at	up	0.096165	guanine nucleotide binding protein (G protein), gamma 4
34755_at	up	0.096176	ADP-ribosyltransferase (NAD <sup>+</sup> ; poly(ADP-ribose) polymerase)-like 2
32708_g_at	down	0.096177	katanin p60 (ATPase-containing) subunit A 1
32228_at	up	0.096212	adaptor-related protein complex 2, alpha 2 subunit
40886_at	down	0.09626	eukaryotic translation elongation factor 1 alpha 1
32285_g_at	up	0.096383	T-box 1
39734_at	down	0.096467	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)
31337_at	up	0.096538	gonadotropin-releasing hormone 2
41488_at	down	0.096667	hypothetical protein A-211C6.1
34438_at	up	0.096753	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9
31478_at	up	0.096764	pancreatic elastase IIB
39867_at	up	0.09692	Tu translation elongation factor, mitochondrial
41324_g_at	up	0.096963	forkhead box M1
1775_at	up	0.097235	
32391_g_at	down	0.097269	polymerase (DNA-directed), alpha (70kD)

40803_at	down	0.097361	pro-oncosis receptor inducing membrane injury gene
34677_f_at	down	0.097379	TL132 protein
493_at	up	0.097484	casein kinase 1, delta
37870_at	up	0.097488	transcription termination factor, RNA polymerase II
41859_at	up	0.097578	uronyl-2-sulfotransferase
37618_at	up	0.097661	homeo box B7
33453_at	up	0.097774	ATPase, H+ transporting, lysosomal interacting protein 1
32909_at	up	0.097796	aquaporin 5
38622_at	up	0.097851	hypothetical protein BC004409
40845_at	down	0.097859	interleukin enhancer binding factor 3, 90kDa
39351_at	down	0.097885	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)
33341_at	down	0.097943	guanine nucleotide binding protein (G protein), beta polypeptide 1
38279_at	up	0.098024	guanine nucleotide binding protein (G protein), alpha z polypeptide
41543_at	up	0.098055	lymphoid nuclear protein related to AF4
41163_at	down	0.09819	integral type I protein
32101_at	down	0.098215	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)
33172_at	up	0.098326	hypothetical protein FLJ10849
36168_at	up	0.098482	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
41385_at	down	0.098533	erythrocyte membrane protein band 4.1-like 3
31537_at	up	0.098538	ADP-ribosyltransferase 1
32564_at	down	0.098647	protein translocation complex beta
1922_g_at	up	0.098667	
158_at	down	0.098748	DnaJ (Hsp40) homolog, subfamily B, member 4
857_at	down	0.099054	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform
34029_at	up	0.099115	dentin matrix acidic phosphoprotein
34544_at	down	0.099119	zinc finger protein 267
35348_at	down	0.099122	protein kinase, AMP-activated, beta 1 non-catalytic subunit
1075_f_at	up	0.099205	interferon, alpha 16
960_g_at	down	0.099331	
35091_at	up	0.099335	neuregulin 2
40785_g_at	down	0.099423	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
1921_at	up	0.099462	
666_at	up	0.099504	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)
33340_at	down	0.099814	paja 2, RING-H2 motif containing
31759_at	up	0.099864	alpha-2 macroglobulin family protein VIP

**EXAMPLE 2: PSYCHIATRIC ILLNESS DIAGNOSIS WITH MULTIGENE  
EXPRESSION CLASSIFICATION****Patient and control subject Recruitment and study procedure**

All subject recruitment was performed according to IRB regulations.

5        ***Medicated Schizophrenia (SZ) Subjects.*** Seven White SZ men between the ages of 25-65 were recruited from the residents of a psychiatric center and four community residential facilities. SZ patients were screened for inclusion based on SZ diagnosis. Patient records from previous admissions and from other facilities were collected for each subject. Informed consent was obtained on the patient's resident ward. Charts were  
10        screened for neuroleptic history and in addition for medical history and other medication use. The seven SZ patients who were analyzed in the preliminary study had medication profiles that were diverse and included several different classes of atypical and typical neuroleptic medications: **Subject 493:** Olanzapine, Depakote, Risperidone., **Subject 494:** Chloral Hydrate, Zyprexa., **Subject 495:** Loxapine, Benztropine, Seroquel, Vistaril.,  
15        **Subject 535:** Clozapine, Artane., **Subject 588:** Haloperidol, Haloperidol Decanoate, Cogentin, Depakote., **Subject 630:** Olanzapine, Risperidone., **Subject 631:** Haloperidol, Clozapine. One patient (ID 494) had been neuroleptic drug-free (Clozapine) a short time (5 days).

20        ***Non-Medication SZ Subject.*** One never-medicated 39-year-old White male SZ subject was recruited into the study, **Subject 964.** Increasing delusions and paranoia precipitated the subject's admission to a local community hospital. He was hospitalized for 37 days but refused all medications. He was assessed for court-mandated treatment but did not fulfill the criteria of dangerousness and this avenue was not pursued. At no time during his hospitalization was any emergency or stat medication administered. The patient was  
25        given an Axis I paranoid schizophrenia diagnosis. His global assessment of functioning score was 28%. The patient's physical examination found no medical conditions or abnormalities, and his SMAC, CBC and urinalysis results were all within the normal ranges. At admission a urine drug toxicology screen proved negative.

30        Informed consent was obtained, and a blood draw was performed. The subject was questioned about his general health, his treatment history and any drug, alcohol and



smoking histories (of which all were negative). A brief psychiatric rating scale (BPRS) was administered and his BPRS score was 43.

**Control Subjects.** Five age-matched controls were recruited from the staff.

Subjects completed a form (with the study team assistance) documenting that neither they  
5 nor their first degree relatives had a history of SZ, other psychotic disorders, mood disorders or of paranoid, schizoid, or schizotypal personality disorder. Subjects were also questioned about their smoking history any current use of, or history of alcohol or illicit drugs. Forms were also completed listing current medications and medical history. Subjects were seen at their place of work and informed consent obtained. Control subjects  
10 were given the study ID nos. 401, 492, 536, 634, and 641).

**BPD Subjects.** Two White male subjects with a diagnosis of BPD (both aged 41), were recruited into the study. Patient records from previous admissions and from other facilities were collected for each subject. Informed consent was obtained on the patient's resident ward. Charts were screened for present and past neuroleptic use and in addition  
15 for medical history exclusions and other medication or drug use and smoker status (as described above). The BPD subjects had medication profiles as follows: **Subject 767:** Depakote, Quetiapine and Zoloft., **Subject 846:** Fluoxetine and Remeron.

**Medical Exclusions.** A list of medical exclusions was generated. A complete blood count (CBC) with differentials was performed for all samples collected <sup>74</sup>.

20 **Sample Processing and Microarray Hybridization.** Immediately after blood collection, leukocytes were isolated by lysis of red cells, centrifugation and washing (Qiagen). Purified leukocytes were stored at -70°C prior to RNA extraction. 8µg of total RNA was employed as a cDNA synthesis template, using an oligo-dT primer and Reverse Transcriptase (RT) enzyme, according to standard Affymetrix protocols. Purified cDNA,  
25 quantified by gel electrophoresis, was then used as a template to generate biotin labeled cRNA, using an *in-vitro* transcription kit (Enzo). cRNA samples were quantified by UV spectrometry and stored at -70°C prior to fragmentation. Following fragmentation, 20ng of each cRNA product was hybridized to an Affymetrix TEST3 array to check the quality of each sample. Each cRNA sample was then hybridized to an HU95A array.

**Real-Time RT-PCR.** 200 ng of total RNA from each subject was employed for first strand cDNA synthesis, using random hexamer primers and Superscript<sup>II</sup> RT enzyme (Invitrogen). Primers were designed using the Primer3 program (Whitehead Institute), except for the 18S ribosomal RNA primers, which were purchased as an internal standard PCR kit (Ambion). For real-time PCR the SYBR Green assay, which measures the linear binding of florescent molecules to double-stranded DNA molecules at each cycle of the amplification, was performed using the Quantitech Kit (Qiagen), on an ABI PRISM 7700 apparatus. The resultant data was imported into Sequence Detector, v1.7a software (ABI), and Cts were calculated. The Ct (the PCR threshold cycle where an increase in reporter fluorescence above a baseline signal can first be detected) has a direct correlation with template concentration. The Ct's of samples with known copy numbers were employed to generate standard amplification curves for each set of specific gene primers. Final copy numbers of each sample RNA were determined from a standard curve, and compared with the 18S standard results.

#### **Gene Expression Data Acquisition and Analysis**

**Affymetrix<sup>®</sup> Microarray Suite Software (v5.0)** Data acquisition was performed as described for Example 1. The resultant data was converted to Excel spreadsheets, and collated. All gene expression values given an "absent call" were removed from the datasets. Gene expression data was then filtered by removing all genes from analysis if they were not found to be "present" in at least two subjects. All statistical tests on the data were performed in Excel, except those described in detail below.

**Data analysis and Hierarchical Clustering.** Heirarchical clustering was performed as described for Example 1, above, using the Cluster program.

#### **Results of the Preliminary Studies**

**Pair-wise Analysis of microarray results.** To investigate total sample variability, a pair-wise comparison of expression levels was performed. It is expected that over 12,000 data points, samples should be highly correlated to allow meaningful comparison of the data. Correlation coefficients were within the range of 0.85-0.93 for each comparison (data not shown). Two samples were processed in duplicate by multiple hybridizations to

HU95A arrays. The reproducibility of the Affymetrix system was illustrated by the  $r^2$  values of 0.97 and 0.99. For

***Analysis of gene expression from genes differentially regulated in peripheral blood***

***leukocytes.*** Genes or protein products previously found to be differentially regulated in  
 5 blood were investigated. The mean and variance of expression levels were calculated  
 across the SZ and Control groups. Altered expression levels (SZ v Controls for each gene)  
 for the dopamine D<sub>3</sub> receptor (+20%), IL-1 receptor antagonist (+30%), IL-2 (-16%),  
 CD3 (+44%), CD4 (+49%), CD8 (+66%), VLA-4 (+33%) and TNF- $\alpha$  (+185%) were  
 found to concur with previously published findings (Ilani et al., Proc Natl Acad Sci U S A  
 10 2001;98(2):625-628; Akiyama. Schizophr Res 1999;37(1), 97-106; Kim, et al., Biol Psychiatry  
 1998;43(9):701-4; Sperner-Unterweger et al., Schizophr Res 1999; 38(1):61-70; Muller et al.,  
 Am J Psychiatry 1999;156(4):634-6; Cazzullo et al., Schizophr Res 1998 31(1):49-55; Naudin et  
 al., Schizophr Res 1997 26(2-3):227-33). Interestingly, found many groups of genes were  
 found that were more significantly altered between the two subject groups, showing the  
 15 power of this microarray approach to identify patterns of differentially regulated genes. A  
 few examples of genes that have previously been implicated in studies of SZ or other  
 psychiatric disorders are; neural cell adhesion molecule (N-CAM), +112%,  $p=.008$ .,  
 GABA-A receptor, +247%,  $p=.0003$ ., L-1 type, calcium channel, +39%,  $p=.03$ ., 14-3-  
 3 protein eta chain, -30%,  $p=.008$ , and Ciliary neurotrophic factor, +144%,  $p=0.005$ .

***Hierarchical Clustering of SZ Subjects from Control Subjects.*** Following filtering  
 of the data, a total of 2635 genes remained for further investigation. It may prove useful to  
 perform a supervised clustering experiment, as surrogate tissue (blood leukocytes) is  
 employed in which differences in the patterns of gene expression from SZ patients  
 compared to control subjects may be more subtle than in tissues such as brain. A two-tailed  
 25 t-test across the 2695 genes expressed in the subject's leukocytes was performed, however,  
 for this analysis the non-medicated subject (Subject 964) was not included.. Of the original  
 2695 genes, 513 were found to have expression values significantly different between the  
 SZ subject group and control group ( $p < 0.05$ ), and 948 were found to have  $p < 0.1$   
 between the two groups. Interestingly, an identical t-test on randomized data was  
 30 performed, where subject samples were randomly placed into one of two groups. This was  
 repeated for multiple permuted datasets, and the mean numbers of differentially regulated

genes calculated. 52 genes were found to be significantly different between the randomized groups ( $p < 0.05$ ), while only 122 genes were found to have  $p < 0.1$ . Thus, randomizing the data results in a vast decrease in the number of genes found to be differentially expressed between subject groups, and may represent the noise of this experimental system.

5 A clustering experiment was implemented on the 948 genes that differentiated between the subject groups ( $p < 0.1$ , medicated SZ and controls), with the inclusion of subject 964 in this analysis. Expression levels of the 948 genes for each subject ( $n = 13$ ), were input into the cluster program and the results visualized in TreeView. Figure 3 shows a partial TreeView figure of the subject cluster results. Two interesting observations were noted, 1)

10 SZ subjects do not appear to cluster based on medication profile, for example, the three SZ subjects receiving Clozapine, (P-494, 535, and 631), do not appear within the same cluster subgroup, while subject 964, a never medicated SZ subject clusters with the SZ group, away from the control subjects., and 2) The smoking status of subjects does not appear to influence the segregation of subjects within the clusters (C-401, 641 and 492 smoke, as do  
15 all medicated SZ subjects, but not SZ subject 964). The results of multiple permutations of intra-subject randomization within the data-sets suggesting that these cluster results are not directed by random expression levels in the microarray datasets (data not shown).

Preliminary analysis for these studies was performed, and we expect that use of larger subject numbers for each group and a more conservative analysis ( $p < 0.05$ ), will allow  
20 further investigation of factors affecting classification of subjects, prior to input into Cluster.

***Concordance of expression of the Never-Medicated SZ Subject with Medicated SZ Subjects.*** When subject 964 was added to the SZ patient subject group for significance testing (two-tailed t-tests), versus the healthy control group, there was a 33 % increase in  
25 the total number of genes that were differentially expressed ( $p < .05$ ) between the 2 subject groups, further indicating the concordance of the neuroleptic naive subject with the remainder of the SZ subject group. Additionally, t-testing between the SZ and control subject group, resulted in decreases in p-value (increased significance) for over 79.5% of the genes previously found to be differentially expressed between subject groups prior to  
30 the inclusion of subject 964.

***Analysis of Leukocyte Gene Expression in SZ and Bipolar Disorder (BPD)***

**Subjects.** For additional data to support this application to investigate leukocyte gene expression profiles for classification of SZ and BPD, two further subjects were recruited and analyzed with a diagnosis of BPD (using the last of the B/START funds). In addition, we have also recruited one subject with major depression into the study. Although that these numbers are very small, this data supports the hypothesis presented herein, and therefore illustrates the value of continuing this investigation.

***Analysis of Gene Expression From Genes Differentially Regulated in Peripheral Blood Leukocytes.***

Expression level data for genes previously found to be differentially regulated in SZ and BPD were investigated. The mean and variance of expression levels were calculated between the groups. Although the data is not statistically significant due to the small subject numbers, transcript levels of TNF- $\alpha$  were  $\sim 100\%$  increased in the SZ versus BPD. Other genes found to be differentially regulated include (SZ v BPD for each gene): IL-1 receptor antagonist (+82%), IL-1 beta (+47%) and dopamine D<sub>3</sub> receptor, (-83%). Many other genes that have also been implicated in psychiatric disorders were found to be differentially expressed between SZ and BPD subjects. For comparison, relative expression of those described above is listed as follows: IL-2 (+92%), CD3 (+42%), CD4 (-25%), CD8 (+36%), N-CAM (+56%), GABA-A receptor (+192%), L-1 type, calcium channel (+32%), 14-3-3 protein eta chain (-79%), and Ciliary neurotrophic factor, (+62%).

***Hierarchical Clustering of SZ and BPD Subjects.*** A supervised analysis was then performed using all genes found to be differentially expressed between the SZ and BPD subjects ( $p < 0.01$ ,  $n = 1002$ ). While this result is not significant, it provides some indication into the likelihood of generating classification profiles when larger subject numbers are employed. The TreeView readout in Figure 4A shows representative samples nodes of similar gene expression (vertical axis), ordered by the total gene expression among the 10 subjects (horizontal axis), where in this example expression levels in the SZ subject samples are lower than in both patients with BPD. The scaled horizontal cluster of subjects (Figure 4B) indicates that distinctive patterns of gene expression can classify subjects into groups as shown by the sub-nodes within the tree diagram. It was observed that based on the overall gene expression of 1002 genes the two BPD patients (BPD-767, 846) clustered into one

discrete sub-node away from the SZ patients. Subjects SZ- 964 and 495 appears to cluster into a separate branch of the tree when compared to the other SZ subjects, and suggests that the use of additional subjects should allow further investigation of the actual sub-groupings within the subject clusters. To perform a preliminary investigation on this clustering result, subject gene expression levels were randomized within the dataset and the resultant data were re-clustered. One example readout is shown in Figure 4, where intra-subject randomization of the data was performed. Figure 5A shows the TreeView readout from the initial clustering of 1002 genes, as described above. Figure 5B shows the TreeView readout generated following analysis of the randomized dataset. The short branch lengths between each node of the dendrogram imply that following randomization, subjects have overall gene expression patterns very similar to each other. The Cluster analysis of the other random data iterations, resulted in TreeView readouts where either the samples remained in the order of input into Cluster, or alternatively branch lengths were observed to be vastly reduced, indicating very minor differences in overall gene expression between subjects. These results may suggest that the separation of subjects into nodes within the TreeView diagram is not due to random gene expression levels in the microarray datasets.

Table 2 shows a list of up- or down-regulated genes from PBLs of the eight schizophrenia subjects.

*Table 2. Schizophrenia Gene Expression Results*

This table includes gene expression profile data from 8 schizophrenic subjects versus 5 control subjects. The table includes the Affymetrix probe-set ID for the HU95Av2 GeneChip array, and also the EASE assignment. The EASE data were included because there are instances where an unknown EST (as referenced to by the Affymetrix probeset ID) has later been characterized by others. However, these curation methods are not 100% accurate.

It is very important to note that the significance levels for the genes/ESTs can change with increasing statistical power from comparing additional samples. Therefore, it may be likely that some genes/ESTs may change in significance.

Affymetrix HU95A version2 probe set ids	mean expression in schizophreni c patients compared to healthy controls	two tailed Students t-test significance	EASE Names ( <a href="http://david.niaid.nih.gov/david/ease.htm">david.niaid.nih.gov/david/ease.htm</a> )
37444_at	up	5.39844E-05	par-6 partitioning defective 6 homolog alpha (C.elegans)
37830_at	up	6.10988E-05	transmembrane 4 superfamily member tetraspan NET-5
1112_g_at	up	6.37745E-05	neural cell adhesion molecule 1
34480_at	up	7.1664E-05	cadherin 16, KSP-cadherin
38736_at	down	0.000100789	WD repeat domain 1
1390_s_at	up	0.000104589	growth hormone releasing hormone
37294_at	down	0.000120464	B-cell translocation gene 1, anti-proliferative
34035_at	up	0.000133975	solute carrier family 10 (sodium/bile acid cotransporter family), member 1
33123_at	down	0.000140899	HRIHFB2206 protein
35527_at	up	0.000163856	calcium channel, voltage-dependent, alpha 2/delta subunit 1
32206_at	up	0.000172847	CDC42 binding protein kinase alpha (DMPK-like)
39428_at	down	0.000182565	lymphocyte adaptor protein
41026_f_at	up	0.000185284	glycophorin B (Includes Ss blood group)
37388_at	up	0.000226625	tissue factor pathway inhibitor 2
38691_s_at	up	0.000249289	surfactant, pulmonary-associated protein C
31700_at	up	0.000257409	G protein-coupled receptor 35
40107_at	up	0.000263914	aldolase C, fructose-bisphosphate
35541_r_at	up	0.000282816	KIAA0506 protein
36441_at	up	0.000286506	
33177_at	up	0.000290145	hypothetical protein MGC4293
1836_at	down	0.000307175	cyclin I
37059_at	up	0.000311251	glucokinase (hexokinase 4) regulatory protein
34178_at	up	0.000352425	zinc finger protein 297
37631_at	up	0.000379094	myosin IE
34011_at	up	0.000383332	harakiri, BCL2 interacting protein (contains only BH3 domain)
31924_at	up	0.000406589	testicular soluble adenylyl cyclase
40354_at	up	0.000434143	heat shock protein (hsp110 family)
39016_r_at	up	0.00044483	keratin 6A
34213_at	up	0.000460936	KIBRA protein

480_at	up	0.000466565	membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase
35952_at	up	0.00048402	
33727_r_at	up	0.000532272	tumor necrosis factor receptor superfamily, member 6b, decoy
32671_at	up	0.000563318	KIAA0173 gene product
41714_at	up	0.000580592	KIAA0455 gene product
36000_at	up	0.000583128	cAMP responsive element binding protein-like 1
37473_at	up	0.000586685	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)
934_at	up	0.00059989	glycosylphosphatidylinositol specific phospholipase D1
35996_at	up	0.00060253	ZW10 interactor anti-sense
38007_at	up	0.000616603	neurofibromin 2 (bilateral acoustic neuroma)
1187_at	up	0.000619655	ligase III, DNA, ATP-dependent
32701_at	up	0.000630146	armadillo repeat gene deletes in velocardiofacial syndrome
33960_s_at	up	0.00065576	calcium channel, voltage-dependent, L type, alpha 1B subunit
37584_at	up	0.000662109	Fanconi anemia, complementation group G
37551_at	up	0.000674595	KIAA0211 gene product
1937_at	up	0.00067796	
33277_at	up	0.000693507	myotubularin related protein 2
36237_at	up	0.000693967	solute carrier family 22 (organic anion transporter), member 6
41377_f_at	up	0.000700545	UDP glycosyltransferase 2 family, polypeptide B7
35858_at	up	0.000706501	postmeiotic segregation increased 2-like 9
31495_at	up	0.000713236	chemokine (C motif) ligand 2
37413_at	up	0.000724544	dipeptidase 1 (renal)
36222_at	up	0.000729569	lymphocyte antigen 6 complex, locus G6C
39279_at	down	0.000742449	bone morphogenetic protein 6
37658_at	up	0.000769593	growth arrest-specific 6
34209_at	up	0.000774852	inositol 1,4,5-trisphosphate 3-kinase C
34963_at	up	0.000798158	collagen, type XIV, alpha 1 (undulin)
41081_at	up	0.00080125	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)
40997_at	up	0.000802266	mitogen-activated protein kinase kinase kinase 12
35384_at	up	0.000812766	histamine receptor H1
268_at	down	0.000882562	platelet/endothelial cell adhesion molecule (CD31 antigen)
35890_at	up	0.000883719	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D



33778_at	up	0.000883921	chromosome 22 open reading frame 4
258_at	up	0.000904043	lymphotoxin alpha (TNF superfamily, member 1)
35219_at	up	0.000908143	hypothetical protein MGC3047
35176_at	up	0.000955593	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)
32162_r_at	up	0.000971421	
31391_at	up	0.001022205	huntingtin-associated protein 1 (neuroan 1)
34479_at	up	0.001039336	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)
738_at	down	0.001062791	5'-nucleotidase, cytosolic II
35719_at	down	0.001077778	pleckstrin homology domain containing, family E (with leucine rich repeats) member 1
236_at	up	0.001119267	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O
33779_at	up	0.001119359	vesicle-associated membrane protein 1 (synaptobrevin 1)
31653_at	up	0.001120702	peter pan homolog (Drosophila)
41644_at	up	0.001148448	KIAA0790 protein
35312_at	up	0.001149439	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)
38202_at	up	0.001170423	FAT tumor suppressor homolog 2 (Drosophila)
1943_at	up	0.001242703	cyclin A2
34894_r_at	up	0.001244784	protease, serine, 22
38162_at	up	0.001251007	regulating synaptic membrane exocytosis 2
689_at	up	0.001251663	paraneoplastic antigen
41694_at	up	0.001259985	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa
31991_at	up	0.0012619	
41507_at	up	0.001276543	mitogen-activated protein kinase-activated protein kinase 5
34949_at	up	0.001318033	adaptor-associated kinase 1
33517_f_at	up	0.001327311	melanoma antigen, family A, 3
41483_s_at	down	0.001346791	jun D proto-oncogene
41641_at	up	0.001347939	GPI-anchored metastasis-associated protein homolog
35313_at	down	0.001365937	KIAA0310 gene product
37779_at	up	0.001386546	acid sphingomyelinase-like phosphodiesterase

38851_at	up	0.001392133	loricrin
1499_at	down	0.001398505	farnesyltransferase, CAAX box, alpha
35197_at	up	0.001406638	
35853_at	up	0.001414183	protein kinase C, alpha binding protein
35932_at	up	0.001424663	left-right determination, factor B
39568_g_at	up	0.001432152	aquaporin 7
32000_g_at	up	0.001434142	ATP-binding cassette, sub-family A (ABC1), member 1
37436_at	up	0.001447929	mitochondrial capsule selenoprotein
34235_at	up	0.001481689	G protein-coupled receptor 116
36907_at	up	0.001501258	mevalonate kinase (mevalonic aciduria)
31882_at	up	0.001503925	RNA, U3 small nucleolar interacting protein 2
36535_at	down	0.001515459	microfibrillar-associated protein 1
1196_at	up	0.001528997	chromosome condensation 1
35505_at	up	0.00152955	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1
41118_at	up	0.001529915	hypothetical protein FLJ13639
34770_at	down	0.001530656	mitogen-activated protein kinase kinase kinase 8
37525_at	up	0.001547367	serine protease inhibitor-like, with Kunitz and WAP domains 1 (eppin)
1285_at	up	0.001552251	
643_at	up	0.001552712	nuclear receptor subfamily 0, group B, member 2
33031_at	up	0.001558992	
37415_at	up	0.001572633	ATPase, Class V, type 10B
38353_at	down	0.001599369	tubulin, gamma complex associated protein 3
32106_at	up	0.001599378	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4
31726_at	up	0.001621904	gamma-aminobutyric acid (GABA) A receptor, alpha 3
38027_at	up	0.001641281	fibulin 1
32420_at	up	0.001677644	G protein-coupled receptor 6
33854_at	down	0.00173595	ATPase, H <sup>+</sup> transporting, lysosomal 34kDa, V1 subunit D
39101_at	up	0.001763484	myosin, heavy polypeptide 2, skeletal muscle, adult
41502_at	up	0.001776846	homeodomain interacting protein kinase 3
39354_at	down	0.001786265	peroxiredoxin 6
39862_at	up	0.00179467	KIAA0296 gene product
38982_at	down	0.001798352	telomeric repeat binding factor 2, interacting protein
33640_at	up	0.001802226	allograft inflammatory factor 1

34131_at	up	0.001817414	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
31686_at	up	0.001831044	tubulin, beta polypeptide 4, member Q
33648_at	up	0.001850125	cholinergic receptor, nicotinic, beta polypeptide 3
35035_at	up	0.001852417	
39570_at	up	0.001878741	hypothetical protein DKFZp434G2311
38125_at	up	0.001882819	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
37978_at	up	0.001896075	quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))
32010_at	up	0.001904026	hypothetical protein EAN57
39609_at	up	0.00193915	single-minded homolog 2 (Drosophila)
39622_at	up	0.001950092	glial cells missing homolog 1 (Drosophila)
38707_r_at	up	0.001970767	E2F transcription factor 4, p107/p130-binding
39520_at	up	0.001987141	KIAA0692 protein
34506_at	up	0.001990895	aminolevulinate, delta-, dehydratase
41771_g_at	up	0.001997028	monoamine oxidase A
36281_at	up	0.002006192	nescient helix loop helix 1
39899_at	up	0.002018086	TSLC1-like 2
262_at	down	0.002038292	adenosylmethionine decarboxylase 1
33281_at	up	0.002042034	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon
36730_at	up	0.002098173	ATP-binding cassette, sub-family C (CFTR/MRP), member 10
40236_at	up	0.002111687	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2
36731_g_at	up	0.002115082	ATP-binding cassette, sub-family C (CFTR/MRP), member 10
282_at	up	0.002123585	M-phase phosphoprotein 1
41647_at	up	0.002129848	STE20-like kinase
33080_s_at	up	0.002156909	RAP1, GTPase activating protein 1
558_at	up	0.002159946	keratin 1 (epidermolytic hyperkeratosis)
39714_at	down	0.002160768	SH3 domain binding glutamic acid-rich protein like
34630_s_at	up	0.002160768	dynein, axonemal, heavy polypeptide 9

41200_at	up	0.002177956	scavenger receptor class B, member 1
40020_at	up	0.002182404	cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila)
37953_s_at	up	0.002214218	amiloride-sensitive cation channel 2, neuronal
34425_at	up	0.002221153	major histocompatibility complex, class I-related
40957_at	down	0.002223327	joined to JAZF1
2046_at	up	0.002238232	
31628_at	up	0.00224761	solute carrier family 15 (oligopeptide transporter), member 1
34590_at	up	0.002247733	ciliary neurotrophic factor
40219_at	up	0.002257582	HMBA-inducible
35502_at	up	0.00228274	anti-Mullerian hormone receptor, type II
32640_at	up	0.00229347	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor
31596_f_at	up	0.0023025	immunoglobulin lambda-like polypeptide 2
35920_at	up	0.00234203	hemoglobin, beta pseudogene 1
41013_at	up	0.002357083	
36084_at	up	0.00236503	KIAA0076 gene product
38171_at	up	0.00238626	WD-repeat protein
41209_at	up	0.002391825	lipoprotein lipase
38858_at	up	0.002394103	potassium voltage-gated channel, subfamily H (eag-related), member 2
40399_r_at	up	0.002401232	mesenchyme homeo box 2 (growth arrest-specific homeo box)
32141_at	up	0.002413611	protein phosphatase 1E (PP2C domain containing)
1681_at	up	0.002427249	estrogen receptor 1
32681_at	up	0.002434539	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na <sup>+</sup> /H <sup>+</sup> , amiloride sensitive)
39097_at	down	0.002438561	SON DNA binding protein
435_g_at	up	0.002444462	H1 histone family, member 0
40400_at	up	0.002448507	adenosine A1 receptor
34704_r_at	up	0.002448849	chorionic somatomammotropin hormone 2
1662_r_at	up	0.002482635	
35448_at	up	0.002497094	peptidylprolyl isomerase (cyclophilin)-like 2
32498_at	up	0.002516445	glutamate receptor, metabotropic 2
34370_at	down	0.002528889	archain 1
396_f_at	up	0.002531111	erythropoietin receptor
1035_g_at	up	0.002533413	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)
38957_at	up	0.00254188	doublecortin and CaM kinase-like 1

35921_at	up	0.002559242	hemoglobin, beta pseudogene 1
873_at	up	0.002587161	homeo box A5
545_g_at	down	0.002588546	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
309_f_at	up	0.002594278	growth hormone 2
1442_at	up	0.002597237	estrogen receptor 2 (ER beta)
1814_at	down	0.002601426	transforming growth factor, beta receptor II (70/80kDa)
37153_at	up	0.002626944	nephronophthisis 4
41807_at	down	0.002629111	sin3-associated polypeptide, 18kDa
38513_at	up	0.00264673	processing of precursors 1
33403_at	down	0.002651277	DKFZP547E1010 protein
786_at	up	0.002669384	polymerase (DNA directed), alpha
31975_at	up	0.002694514	
38495_s_at	up	0.00271851	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included)
714_at	up	0.002720175	
38482_at	up	0.00272614	claudin 7
1967_f_at	up	0.002739683	
39240_at	up	0.002744223	neurexin 1
37575_at	down	0.002760815	
1063_s_at	up	0.0027749	TYRO3 protein tyrosine kinase
31590_g_at	up	0.002776136	
37898_r_at	up	0.002781402	trefoil factor 3 (intestinal)
37983_at	up	0.002787601	angiotensin II receptor, type 1
37273_at	up	0.002809352	
926_at	up	0.002825805	metallothionein 1G
34293_at	up	0.002829536	kinesin family member C3
33821_at	down	0.00283335	homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2
36840_at	up	0.002837181	hypothetical protein FLJ10737
31889_at	up	0.002846254	melan-A
37151_at	up	0.002860716	
32201_at	up	0.002868158	Sjogren's syndrome nuclear autoantigen 1
414_at	up	0.002884861	homeo box D10
35520_at	up	0.002889864	claudin 9
39666_at	up	0.002894488	guanine nucleotide binding protein (G protein), gamma 4
38621_at	up	0.002895693	dimethylarginine dimethylaminohydrolase 2
970_r_at	up	0.002920493	ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila)
41247_at	up	0.002926933	
1022_f_at	up	0.002930839	interferon, alpha 14

41500_at	up	0.002932033	v-ski sarcoma viral oncogene homolog (avian)
34679_at	up	0.002938559	breakpoint cluster region
33942_s_at	up	0.002939961	syntaxin binding protein 1
33454_at	up	0.002954371	agrin
32048_at	up	0.002956969	
39567_at	up	0.002960606	aquaporin 7
734_at	up	0.003021185	
40473_at	down	0.003051481	serine/threonine kinase 24 (STE20 homolog, yeast)
160029_at	down	0.003081574	protein kinase C, beta 1
37097_at	up	0.003086294	solute carrier family 17 (sodium phosphate), member 1
32172_at	down	0.003088013	SMART/HDAC1 associated repressor protein
38604_at	up	0.003091956	neuropeptide Y
34621_at	up	0.003098553	keratin 2A (epidermal ichthyosis bullosa of Siemens)
32349_at	up	0.003130675	annexin A10
38928_r_at	up	0.003143861	tyrosinase (oculocutaneous albinism IA)
1988_at	up	0.003144002	platelet-derived growth factor receptor, alpha polypeptide
1494_f_at	up	0.003151857	cytochrome P450, family 2, subfamily A, polypeptide 6
32156_at	up	0.003158238	poliovirus receptor-related 2 (herpesvirus entry mediator B)
34440_at	up	0.00317265	DiGeorge syndrome critical region gene 9
37853_at	up	0.003195503	urocortin
39839_at	down	0.003202074	cold shock domain protein A
38747_at	up	0.003205975	CD34 antigen
40565_at	up	0.003225285	apolipoprotein E
31326_at	up	0.003229141	
40668_s_at	up	0.003236501	CD6 antigen
32923_r_at	up	0.003262936	synapsin I
33972_r_at	up	0.003267304	deleted in azoospermia-like
2027_at	up	0.003272896	S100 calcium binding protein A2
38038_at	up	0.003272965	lumican
34820_at	up	0.003338528	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)
34197_at	up	0.003357164	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
41427_at	up	0.003380281	wingless-type MMTV integration site family, member 11

52710_at	up	0.003400348	potassium voltage-gated channel, shaker-related subfamily, beta member 1
192_at	down	0.003400695	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa
34821_at	down	0.003403862	chromosome 6 open reading frame 80
33712_at	up	0.003430688	sulfotransferase family 4A, member 1
37588_s_at	up	0.003433268	mitogen-activated protein kinase 8 interacting protein 2
37372_at	up	0.003438532	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)
40372_at	up	0.003447837	pancreatic lipase-related protein 1
441_s_at	up	0.003458549	leukemia inhibitory factor (cholinergic differentiation factor)
1849_s_at	down	0.003460555	retinoblastoma binding protein 1
541_g_at	up	0.003461606	heat shock 27kDa protein 2
32443_at	up	0.003463616	zinc finger protein 157 (HZF22)
121_at	up	0.003467949	paired box gene 8
41817_g_at	up	0.00349005	caspase recruitment domain family, member 10
39242_at	up	0.003510672	synaptotagmin V
37687_i_at	up	0.003516194	Fc fragment of IgG, low affinity IIa, receptor for (CD32)
40302_at	up	0.003521173	emilin and multimerin-domain containing protein 1
39192_at	up	0.003526575	tumor necrosis factor receptor superfamily, member 17
39722_at	up	0.003536214	nuclear receptor co-repressor 1
31936_s_at	down	0.003552058	limkain b1
32407_f_at	up	0.003585808	
36304_at	up	0.00359153	complement component 8, beta polypeptide
37270_at	up	0.003593677	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 2 polypeptide
40171_at	down	0.003618084	frequently rearranged in advanced T-cell lymphomas 2
39495_at	up	0.003639204	hypothetical protein FLJ20719
37139_at	up	0.003644433	ectodermal dysplasia 1, anhidrotic
31681_at	up	0.003648646	erythropoietin receptor
41276_at	up	0.003680784	sin3-associated polypeptide, 18kDa
36469_at	up	0.003682865	dystrobrevin, alpha
32810_at	up	0.003706452	thiopurine S-methyltransferase
34069_s_at	up	0.003710418	synovial sarcoma translocation, chromosome 18
37087_at	up	0.003723312	A kinase (PRKA) anchor protein 4
32513_at	up	0.003730609	neurofilament 3 (150kDa medium)

614_at	up	0.003737015	phospholipase A2, group IIA (platelets, synovial fluid)
1019_g_at	up	0.003737542	wingless-type MMTV integration site family, member 10B
36123_at	down	0.003760113	thiosulfate sulfurtransferase (rhodanese)
33211_at	up	0.003774765	ribosome binding protein 1 homolog 180kDa (dog)
38541_at	up	0.003778747	cytochrome P450, family 21, subfamily A, polypeptide 2
39343_at	up	0.003780079	transformer-2 alpha (htra-2 alpha)
36888_at	up	0.00379196	KIAA0841 protein
37312_at	down	0.003803597	transcriptional regulator interacting with the PHS-bromodomain 2
37785_at	up	0.003817423	GTP-binding protein
33323_r_at	up	0.003818801	stratifin
35633_at	down	0.003823077	engulfment and cell motility 1 (ced-12 homolog, C. elegans)
34273_at	up	0.003831402	regulator of G-protein signalling 4
35545_at	up	0.003835274	solute carrier family 4, sodium bicarbonate cotransporter, member 8
33661_at	up	0.003844513	ribosomal protein L5
40359_at	up	0.003849677	chromosome 11 open reading frame 13
37056_at	up	0.003860515	tec protein tyrosine kinase
33268_at	up	0.003860581	Smcx homolog, X chromosome (mouse)
37618_at	up	0.003865292	homeo box B7
36323_at	up	0.003868425	gamma-aminobutyric acid (GABA) A receptor, alpha 1
31654_at	up	0.003872787	VPS10 domain receptor protein SORCS 3
39990_at	up	0.003883048	ISL1 transcription factor, LIM/homeodomain, (islet-1)
38608_at	up	0.003891136	lectin, galactoside-binding, soluble, 7 (galectin 7)
35746_r_at	down	0.003899767	poly(rC) binding protein 2
259_s_at	up	0.003922965	tumor necrosis factor (TNF superfamily, member 2)
34558_at	up	0.00393898	opiate receptor-like 1
34457_at	up	0.003943871	solute carrier family 30 (zinc transporter), member 3
31771_at	up	0.003954233	
32292_at	up	0.003968658	collectin sub-family member 10 (C-type lectin)
32171_at	down	0.003976408	eukaryotic translation initiation factor 5
37166_at	up	0.004008678	3-hydroxyanthranilate 3,4-dioxygenase



1012_s_at	down	0.004008843	jun D proto-oncogene
38636_at	up	0.004009285	immunoglobulin superfamily containing leucine-rich repeat
39939_at	up	0.004024305	collagen, type IV, alpha 6
39459_at	up	0.004034943	ribosomal protein S13
41437_at	down	0.004042248	chromosome 14 open reading frame 109
872_i_at	up	0.00408932	insulin receptor substrate 1
39091_at	down	0.004093417	vitamin A responsive; cytoskeleton related
35319_at	down	0.004100726	CCCTC-binding factor (zinc finger protein)
33967_at	up	0.004109676	major histocompatibility complex, class II, DO alpha
333_s_at	down	0.004110914	
39400_at	up	0.00412939	KIAA1055 protein
39304_g_at	up	0.004129597	beta-transducin repeat containing
37838_at	up	0.004143313	coagulation factor XII (Hageman factor)
35970_g_at	down	0.00414378	M-phase phosphoprotein 9
1669_at	up	0.004147458	wingless-type MMTV integration site family, member 5A
38822_at	up	0.004163563	serine/threonine kinase 17a (apoptosis-inducing)
145_s_at	up	0.004167288	T-box 5
38883_at	up	0.004187484	
39917_at	up	0.004214466	tubulin, gamma complex associated protein 2
32650_at	up	0.004216408	neuronal protein
35007_at	down	0.004227977	
41655_at	up	0.004234936	midline 2
37731_at	down	0.004243561	epidermal growth factor receptor pathway substrate 15
34066_at	up	0.004275892	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
33885_at	down	0.004286872	KIAA0907 protein
37025_at	down	0.004312041	lipopolysaccharide-induced TNF factor
35699_at	up	0.004318144	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)
36129_at	up	0.004340344	KIAA0397 gene product
32629_f_at	up	0.004351049	butyrophilin, subfamily 3, member A1
40625_f_at	up	0.004352482	metaxin 1
37465_at	up	0.004357604	brain-specific protein p25 alpha
1700_at	up	0.00436827	BCL2 binding component 3
32345_at	up	0.00437274	

35281_at	up	0.004383388	laminin, gamma 2
32358_at	up	0.004391543	WNT1 inducible signaling pathway protein 3
32007_at	up	0.004446678	
35803_at	up	0.004448806	ras homolog gene family, member E
35630_at	up	0.004449475	lethal giant larvae homolog 2 (Drosophila)
33467_at	up	0.004454387	CMRF35 leukocyte immunoglobulin-like receptor
41449_at	up	0.004456743	sarcoglycan, epsilon
1075_f_at	up	0.004457857	interferon, alpha 16
1567_at	up	0.004477979	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
32223_at	up	0.004484703	splicing factor, arginine/serine-rich 14
35745_f_at	down	0.004489339	poly(rC) binding protein 2
32888_at	up	0.00451066	leukocyte tyrosine kinase
1777_at	up	0.004521209	Ras and Rab interactor 1
40042_r_at	up	0.004524196	proline dehydrogenase (oxidase) 1
35896_at	up	0.004592292	DKFZp434P211 protein
34702_f_at	up	0.004610914	chorionic somatomammotropin hormone 2
1339_s_at	up	0.004621845	breakpoint cluster region
1799_at	up	0.004625646	excision repair cross-complementing rodent repair deficiency, complementation group 4
35320_at	up	0.004625842	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2
37191_at	up	0.00462609	phytanoyl-CoA hydroxylase interacting protein
33521_at	up	0.004640954	ATPase, H <sup>+</sup> /K <sup>+</sup> exchanging, alpha polypeptide
34527_r_at	up	0.004649009	
34467_g_at	up	0.004656371	5-hydroxytryptamine (serotonin) receptor 4
37760_at	up	0.004663199	BAI1-associated protein 2
33418_at	down	0.004726336	
39720_g_at	up	0.00473358	zona pellucida glycoprotein 3 (sperm receptor)
32028_at	up	0.004738157	phosphomannomutase 2
35666_at	up	0.004741066	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F
31591_s_at	up	0.004769075	complement factor H-related 4

39009_at	down	0.004782089	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)
38847_at	up	0.004785318	maternal embryonic leucine zipper kinase
37793_r_at	up	0.004797672	RAD51-like 3 (S. cerevisiae)
32837_at	up	0.004799361	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
32092_at	up	0.004804199	syndecan 3 (N-syndecan)
35307_at	down	0.004819968	GDP dissociation inhibitor 2
34141_at	up	0.004824997	
40321_at	up	0.004840659	interleukin 1 receptor-like 1
40622_r_at	up	0.004881409	ubiquitin protein ligase
39128_r_at	up	0.004896276	protein phosphatase 2A, regulatory subunit B' (PR 53)
36819_at	up	0.004902066	Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3)
36702_at	up	0.004916649	T-box 19
1828_s_at	up	0.004940536	fibroblast growth factor 2 (basic)
33047_at	up	0.004989688	
41192_at	down	0.004996772	hypothetical protein 669
33134_at	up	0.005003649	adenylate cyclase 3
564_at	up	0.005026874	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
38797_at	up	0.005038875	KIAA0062 protein
40276_at	down	0.005046073	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)
40199_at	up	0.005054057	msh homeo box homolog 1 (Drosophila)
31818_at	up	0.005058057	
1832_at	up	0.00506241	mutated in colorectal cancers
39051_at	up	0.005064802	neuronatin
31676_at	up	0.005081672	zinc finger protein 208
32479_at	up	0.005105492	tumor necrosis factor receptor superfamily, member 11a, activator of NFkB
39197_s_at	up	0.005111726	
39750_at	up	0.005142581	zinc finger, DHHC domain containing 3
39986_at	up	0.005154791	hepatocellularcarcinoma-associated antigen HCA557a
37053_at	up	0.005195125	ATPase, Ca++ transporting, plasma membrane 2
32389_at	up	0.005199094	RNA, U2 small nuclear

40376_at	up	0.005209375	arylsulfatase E (chondrodysplasia punctata 1)
1379_at	up	0.005219489	EphA2
38440_s_at	down	0.005255831	hypothetical protein FLJ20811
33520_at	up	0.005264186	coagulation factor VII (serum prothrombin conversion accelerator)
39688_at	up	0.00527689	requiem, apoptosis response zinc finger gene
31829_r_at	up	0.005284494	trans-golgi network protein 2
2066_at	up	0.005318536	BCL2-associated X protein
38294_at	up	0.005318622	homeo box D4
32971_at	up	0.00533295	Friedreich ataxia region gene X123
32509_at	up	0.005359441	HBxAg transactivated protein 2
41227_at	up	0.00537468	oculocerebrorenal syndrome of Lowe
41840_r_at	up	0.005385137	
1804_at	up	0.005407113	kallikrein 3, (prostate specific antigen)
34703_f_at	up	0.005425622	chorionic somatomammotropin hormone 2
34060_g_at	up	0.005447522	Pvt1 oncogene homolog, MYC activator (mouse)
39499_s_at	up	0.005466238	par-3 partitioning defective 3 homolog (C. elegans)
32240_at	up	0.005479107	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5.
31817_at	up	0.005494234	gamma-aminobutyric acid (GABA) A receptor, beta 3
32077_s_at	up	0.005543575	potassium voltage-gated channel, KQT-like subfamily, member 1
33762_r_at	up	0.005564914	KIAA0493 protein
37459_at	up	0.005565205	collagen, type VIII, alpha 1
1240_at	up	0.00556878	caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2)
33711_at	up	0.00557075	proopiomelanocortin (adrenocorticotropin/ beta-lipotropin/ alpha-melanocyte stimulating hormone/ beta-melanocyte stimulating hormone/ beta-endorphin)
31411_at	up	0.005579666	variable charge, Y chromosome, 2
36337_at	up	0.005593633	KIAA0963 protein
40340_at	up	0.005596156	hypothetical protein DKFZp586E1923
35536_at	up	0.005620504	endothelin converting enzyme 2
33000_at	up	0.005629213	hepatitis A virus cellular receptor 1
34906_g_at	up	0.005635263	glutamate receptor, ionotropic, kainate 5
37721_at	up	0.005646504	deoxyhypusine synthase

32642_at	up	0.005651069	chondroitin sulfate proteoglycan 3 (neurocan)
39160_at	down	0.005660176	pyruvate dehydrogenase (lipoamide) beta
41264_at	up	0.005670964	
34655_at	up	0.0057165	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)
31861_at	up	0.005718235	immunoglobulin mu binding protein 2
36734_at	up	0.005753457	small proline-rich protein 2A
39310_at	up	0.005754564	bradykinin receptor B2
770_at	up	0.005756245	glutathione peroxidase 3 (plasma)
764_s_at	up	0.005789206	clock homolog (mouse)
31350_at	up	0.005792228	olfactory receptor, family 10, subfamily H, member 3
40615_at	down	0.005797033	hypothetical protein FLJ21439
38180_f_at	up	0.005826003	pregnancy specific beta-1-glycoprotein 9
33574_at	up	0.005842528	chromosome 6 open reading frame 10
33986_r_at	up	0.005846995	heat shock 90kDa protein 1, beta
31542_at	up	0.005886628	filaggrin
36578_at	down	0.005897302	baculoviral IAP repeat-containing 2
31442_at	up	0.005902455	
37839_at	up	0.005906266	
39445_at	up	0.005922975	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3
41046_s_at	up	0.00592598	zinc finger protein 261
36546_r_at	up	0.005940762	KIAA0542 gene product
40907_at	up	0.005948234	hypothetical protein FLJ32130
160020_at	up	0.005967887	matrix metalloproteinase 14 (membrane-inserted)
41793_at	up	0.005969246	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
35899_at	up	0.00598163	artemin
41354_at	up	0.005996623	stanniocalcin 1
731_f_at	up	0.006023842	
41051_at	down	0.006083685	translin-associated factor X
39598_at	up	0.006099426	gap junction protein, beta 1, 32kDa (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked)
40877_s_at	up	0.006100957	D15F37 (pseudogene)
39619_at	up	0.006107927	SGC32445 protein
40554_at	up	0.006116743	golgi phosphoprotein 4
548_s_at	down	0.006131531	spleen tyrosine kinase
230_s_at	up	0.00614997	follicle stimulating hormone, beta polypeptide
35637_at	up	0.006154739	hypothetical protein PRO2325
32241_at	down	0.006160593	TAR DNA binding protein

2077_at	up	0.006189769	integrin, alpha 6
40825_at	up	0.00622426	microtubule-associated protein, RP/EB family, member 3
39472_s_at	up	0.006239579	BRAF35/HDAC2 complex (80 kDa)
38320_s_at	up	0.006246922	lipase, hormone-sensitive
37972_at	up	0.006252496	deoxyribonuclease I-like 3
31410_at	up	0.006253494	tumor necrosis factor receptor superfamily, member 13B
33594_at	up	0.006264788	dickkopf homolog 4 ( <i>Xenopus laevis</i> )
40081_at	up	0.00627529	phospholipid transfer protein
34301_r_at	up	0.006279415	keratin 17
35329_at	down	0.006296693	cytochrome b5 reductase 1 (B5R.1)
31709_at	up	0.006341656	nuclear receptor co-repressor 2
34415_at	up	0.006342999	activin A receptor, type IB
31406_at	up	0.006344356	G protein-coupled receptor 50
35254_at	up	0.006348896	FLN29 gene product
31930_f_at	up	0.006378393	Rhesus blood group, CcEe antigens
38460_at	up	0.006382402	cytochrome b-5
31537_at	up	0.006385628	ADP-ribosyltransferase 1
33538_at	up	0.006387439	myelin expression factor 2
916_at	up	0.006393536	protein tyrosine phosphatase, receptor type, N
35599_at	up	0.006406575	glycine N-methyltransferase
35950_at	up	0.006461703	synovial sarcoma, X breakpoint 4
38468_at	up	0.006474053	Hermansky-Pudlak syndrome 1
1792_g_at	up	0.006476549	cyclin-dependent kinase 2
33064_at	up	0.006495075	calcium channel, voltage-dependent, gamma subunit 1
1680_at	up	0.006503388	growth factor receptor-bound protein 7
34429_at	up	0.006513609	mucosal vascular addressin cell adhesion molecule 1
36600_at	down	0.006518042	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
34108_g_at	up	0.006518826	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2
36727_at	up	0.006526838	erythrocyte membrane protein band 4.1-like 2
732_f_at	up	0.006547759	
31668_f_at	up	0.006549214	
33784_at	up	0.006564337	TNF receptor-associated factor 2
40570_at	down	0.006567141	forkhead box O1A (rhabdomyosarcoma)
34853_at	up	0.006610556	fibronectin leucine rich transmembrane protein 2
571_at	down	0.006623427	nucleosome assembly protein 1-like 1

33532_at	up	0.006633032	cartilage paired-class homeoprotein 1
38597_f_at	up	0.00663979	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
31534_at	up	0.006657321	zinc finger protein, Y-linked
35248_at	up	0.006666707	solute carrier family 19 (thiamine transporter), member 2
35938_at	down	0.006675236	phospholipase A2, group IVA (cytosolic, calcium-dependent)
32430_at	up	0.006677844	gastrin-releasing peptide receptor
35923_at	up	0.006705555	cholecystokinin B receptor
40145_at	up	0.006774519	topoisomerase (DNA) II alpha 170kDa
35013_at	up	0.006804943	lipopolysaccharide binding protein
35898_at	up	0.00681255	WNT1 inducible signaling pathway protein 2
41331_at	up	0.006837963	leucine-rich repeats and immunoglobulin-like domains 2
34308_at	down	0.006842048	histone 1, H2ac
34795_at	up	0.006845198	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
38205_at	up	0.006846391	neurogenic differentiation 2
739_at	up	0.006849272	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)
1208_at	up	0.006860724	PTK6 protein tyrosine kinase 6
38237_at	up	0.006873965	gamma-glutamyltransferase-like activity 1
37061_at	up	0.006878942	chitinase 1 (chitotriosidase)
31897_at	up	0.006912079	downregulated in ovarian cancer 1
34259_at	up	0.006921783	KIAA0664 protein
33510_s_at	up	0.006943429	glutamate receptor, metabotropic 1
37547_at	up	0.006943934	PTH-responsive osteosarcoma B1 protein
38032_at	up	0.006964957	synaptic vesicle glycoprotein 2A
41799_at	up	0.006993973	DnaJ (Hsp40) homolog, subfamily C, member 7
775_at	up	0.00699531	5-hydroxytryptamine (serotonin) receptor 1B
34175_r_at	up	0.00700068	
36833_at	down	0.007015057	galactosidase, alpha
34405_at	up	0.007020147	ubiquitin specific protease 5 (isopeptidase T)
31745_at	up	0.007034964	mucin 3A, intestinal
38507_at	up	0.007046638	cytochrome P450, family 2, subfamily D, polypeptide 6
38504_at	up	0.00705255	calpain 5
31921_at	up	0.007070315	olfactory receptor, family 2, subfamily F, member 1
715_s_at	up	0.007073157	gamma-glutamyltransferase 1

214_at	up	0.007077911	msh homeo box homolog 1 (Drosophila)
41833_at	up	0.007130788	jumping translocation breakpoint
36883_at	up	0.007136738	keratin 13
36404_at	up	0.007145174	glucagon-like peptide 1 receptor
799_at	up	0.007165141	cyclin-dependent kinase 5, regulatory subunit 1 (p35)
39805_at	up	0.00717185	ATP-binding cassette, sub-family B (MDR/TAP), member 6
38136_at	up	0.007176078	Werner syndrome
38193_at	up	0.007185711	immunoglobulin kappa constant
37939_at	up	0.007225072	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C
265_s_at	up	0.00723378	selectin E (endothelial adhesion molecule 1)
39196_i_at	up	0.007240769	leucine-rich repeats and immunoglobulin-like domains 1
37129_at	up	0.007242263	neuropeptide FF-amide peptide precursor
35243_at	up	0.007262299	PCTAIRE protein kinase 3
34167_s_at	up	0.007272108	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7
40523_at	up	0.007280257	forkhead box A2
1925_at	up	0.007284827	cyclin F
41340_at	up	0.00729114	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A
911_s_at	down	0.007294306	calmodulin 2 (phosphorylase kinase, delta)
1463_at	down	0.007297165	protein tyrosine phosphatase, non-receptor type 12
35816_at	down	0.007313124	cystatin B (stefin B)
34061_at	up	0.00731512	Pvt1 oncogene homolog, MYC activator (mouse)
363_at	up	0.007332831	protein kinase C, gamma
AFFX-BioC-3_at	up	0.007343487	
37638_at	up	0.007365403	dedicator of cyto-kinesis 1
37778_at	down	0.007365593	KIN, antigenic determinant of recA protein homolog (mouse)
36252_at	up	0.007369173	cardiotrophin 1
33568_at	up	0.007372628	cholinergic receptor, nicotinic, beta polypeptide 4
37432_g_at	up	0.007374815	Msx-interacting-zinc finger
35317_at	down	0.007374906	meningioma expressed antigen 5 (hyaluronidase)
1100_at	down	0.007398264	interleukin-1 receptor-associated kinase 1



31841_at	up	0.007402655	catenin (cadherin-associated protein), alpha 2
34754_at	up	0.007404094	ezrin-binding partner PACE-1
921_s_at	up	0.007411006	
39099_at	down	0.007442413	Sec23 homolog A (S. cerevisiae)
32998_at	up	0.007466948	cholecystokinin A receptor
34752_at	down	0.007502681	NIMA (never in mitosis gene a)-related kinase 7
37906_at	up	0.007506317	latent transforming growth factor beta binding protein 2
32305_at	up	0.007531192	collagen, type I, alpha 2
32222_at	up	0.007545106	hypothetical protein FLJ14639
33067_at	up	0.007558906	histone 1, H1a
34680_s_at	down	0.007566871	KIAA0107 gene product
602_s_at	up	0.00758131	hydroxysteroid (17-beta) dehydrogenase 1
34466_at	up	0.007587165	5-hydroxytryptamine (serotonin) receptor 4
36790_at	down	0.007671431	tropomyosin 1 (alpha)
35000_at	up	0.007695054	tumor necrosis factor (ligand) superfamily, member 9
41619_at	up	0.007696786	interferon regulatory factor 6
33351_at	down	0.007707386	translation factor sui1 homolog
34406_at	up	0.007730668	KIAA0602 protein
118_at	up	0.007740152	inositol 1,4,5-trisphosphate 3-kinase A
34315_at	up	0.007744077	AFG3 ATPase family gene 3-like 2 (yeast)
39241_at	up	0.007758585	carbonic anhydrase I
1475_s_at	up	0.007800059	v-myb myeloblastosis viral oncogene homolog (avian)
39694_at	up	0.00783975	hypothetical protein MGC5508
272_at	up	0.007842252	gastrin-releasing peptide
1827_s_at	up	0.007852219	v-myc myelocytomatosis viral oncogene homolog (avian)
32592_at	up	0.007864197	KIAA0323 protein
40844_at	down	0.007876275	SH2 domain binding protein 1 (tetra-ricopeptide repeat containing)
35445_at	up	0.00787895	sorting nexin 26
35738_at	down	0.007881499	high mobility group nucleosomal binding domain 4
35306_at	down	0.007886283	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15
33016_at	up	0.007891585	
34359_at	down	0.007895012	CGI-130 protein
37683_at	down	0.007902912	ubiquitin specific protease 10
40943_at	up	0.007973159	long-chain fatty-acyl elongase
882_at	up	0.007997396	colony stimulating factor 1 (macrophage)
40160_at	down	0.007999975	POM121 membrane glycoprotein (rat)

34845_at	up	0.008026503	CGI-51 protein
41076_at	up	0.008027637	gap junction protein, beta 3, 31kDa (connexin 31)
40406_at	up	0.00804141	macrophage stimulating, pseudogene 9
34296_at	up	0.008078528	midline 1 (Opitz/BBB syndrome)
33866_at	down	0.008090063	tropomyosin 4
33493_at	up	0.008093623	erythroid differentiation and denucleation factor 1
37407_s_at	up	0.008123032	myosin, heavy polypeptide 11, smooth muscle
33707_at	up	0.008136505	phospholipase A2, group IVC (cytosolic, calcium-independent)
31609_s_at	up	0.00813732	procollagen C-endopeptidase enhancer
38991_at	up	0.008149715	KIAA0220 protein
34773_at	down	0.008173332	tubulin-specific chaperone a
39262_at	up	0.008173678	protein predicted by clone 23627
1116_at	up	0.008206557	CD19 antigen
863_g_at	up	0.008219712	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5
35340_at	down	0.008224703	mel transforming oncogene (derived from cell line NK14)- RAB8 homolog
34367_at	up	0.00822972	phosphoglycerate dehydrogenase
36585_at	down	0.008245871	ADP-ribosylation factor 4
33105_at	up	0.008266479	pleckstrin homology domain containing, family B (evectins) member 1
33169_at	up	0.008284475	neogenin homolog 1 (chicken)
40161_at	up	0.008318429	cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple)
38816_at	up	0.008319784	transforming, acidic coiled-coil containing protein 2
38687_at	down	0.008331445	DKFZP566D193 protein
34662_at	up	0.008344705	myc-induced nuclear antigen, 53 kDa
38400_at	down	0.008348744	DKFZP434D1335 protein
38052_at	down	0.008362106	coagulation factor XIII, A1 polypeptide
34556_at	up	0.008416122	keratin 9 (epidermolytic palmoplantar keratoderma)
39662_s_at	up	0.008428792	G protein-coupled receptor kinase 2-like (Drosophila)
32188_at	up	0.008428989	myelin transcription factor 1
36684_at	down	0.008431467	adenosylmethionine decarboxylase 1
34436_at	up	0.008455809	solute carrier family 17 (sodium phosphate), member 3
38607_at	up	0.008486615	transmembrane 4 superfamily member 5
41428_at	up	0.008492173	ATP-binding cassette, sub-family C (CFTR/MRP), member 5

31923_f_at	up	0.008506636	ubiquilin 2
34365_at	up	0.008508922	peptidylprolyl isomerase E (cyclophilin E)
36242_at	up	0.008513005	small proline-rich protein 2C
38132_at	up	0.008552125	CDC42 effector protein (Rho GTPase binding) 1
1177_at	up	0.008558202	
36706_at	up	0.008564806	cyclin-dependent kinase-like 5
41021_s_at	up	0.0085664	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
38067_at	up	0.008583304	likely ortholog of mouse septin 8
33740_at	up	0.00860968	chromosome 1 open reading frame 2
1167_s_at	up	0.008638816	matrix metalloproteinase 15 (membrane-inserted)
1726_at	up	0.008668644	
40847_at	up	0.008669583	flavoprotein oxidoreductase MICAL2
37368_at	up	0.008705091	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
40277_at	up	0.008712834	golgi associated, gamma adaptin ear containing, ARF binding protein 2
35955_at	up	0.008714371	cytochrome c-like antigen
41233_at	down	0.008722182	DnaJ (Hsp40) homolog, subfamily B, member 6
40649_at	up	0.008763293	proprotein convertase subtilisin/kexin type 1
36338_at	up	0.008782835	leucine zipper protein 1
35194_at	up	0.008788982	glutathione peroxidase 2 (gastrointestinal)
40304_at	up	0.008813094	bullous pemphigoid antigen 1, 230/240kDa
34559_at	up	0.008828164	
34753_at	down	0.008836314	synaptobrevin-like 1
40834_at	up	0.008856926	PDZ domain containing 3
1025_g_at	up	0.008860423	cytochrome P450, family 1, subfamily A, polypeptide 1
31352_at	up	0.008862037	
38050_at	down	0.008880693	Bcl-2-associated transcription factor
33072_at	up	0.008883812	hypocretin (orexin) receptor 2
41792_at	up	0.00888827	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
35492_at	up	0.008900509	cytochrome P450, family 4, subfamily F, polypeptide 12
707_s_at	up	0.008954052	
678_at	up	0.00896	alkaline phosphatase, placental-like 2
39633_at	up	0.008965521	S100 calcium binding protein A3
35379_at	up	0.008977482	collagen, type IX, alpha 1
38217_at	up	0.00898785	carboxyl ester lipase (bile salt-stimulated lipase)
33788_at	down	0.00901526	lysosomal apyrase-like 1

454_at	up	0.009032927	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1
466_at	down	0.00903801	general transcription factor II, i
1030_s_at	down	0.009041555	topoisomerase (DNA) I
39198_s_at	up	0.00906008	CGI-87 protein
40529_at	up	0.009060975	LIM homeobox protein 2
32098_at	up	0.009061067	collagen, type VI, alpha 2
37981_at	up	0.009065909	drebrin 1
36103_at	up	0.009068444	chemokine (C-C motif) ligand 3
40389_at	up	0.009068618	solute carrier family 38, member 3
40423_at	up	0.009110888	KIAA0903 protein
37885_at	up	0.009118294	hypothetical protein AF038169
39308_r_at	up	0.009130611	clathrin, light polypeptide (Lcb)
39468_r_at	up	0.009165844	
34458_at	up	0.009174722	S100 calcium binding protein A7 (psoriasin 1)
39583_at	up	0.009175879	glioma amplified on chromosome 1 protein (leucine-rich)
34816_at	down	0.009179229	E1A binding protein p400
35275_at	up	0.009197426	adaptor-related protein complex 1, gamma 1 subunit
170_at	up	0.009214034	caudal type homeo box transcription factor 2
38059_g_at	up	0.009215265	dermatopontin
40501_s_at	up	0.00921917	myosin binding protein C, slow type
32372_at	up	0.00922417	cathepsin B
1957_s_at	up	0.009230348	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)
123_at	up	0.009235174	protein kinase C, mu
39150_at	down	0.009258766	ring finger protein 11
36813_at	up	0.009266999	thyroid hormone receptor interactor 13
38758_at	up	0.009277164	PDGFA associated protein 1
32198_at	up	0.009286085	hypothetical protein FLJ20452
39667_at	up	0.009305838	neuro-oncological ventral antigen 2
1796_s_at	up	0.009311292	B-cell CLL/lymphoma 3
35279_at	down	0.009332113	Tax1 (human T-cell leukemia virus type I) binding protein 1
32405_at	up	0.009349281	thioesterase, adipose associated
31785_f_at	up	0.009376814	unnamed HERV-H protein
41458_at	up	0.009388812	KIAA0467 protein
34443_at	up	0.009406186	

31324_at	up	0.009411243	
32303_at	up	0.00943436	ets variant gene 3
32915_at	up	0.00943445	
37004_at	up	0.009438749	surfactant, pulmonary-associated protein B
35481_at	up	0.009450411	myosin heavy chain Myr 8
33282_at	up	0.009471432	ladinin 1
41307_at	up	0.009526397	CCR4-NOT transcription complex, subunit 2
39238_at	up	0.009533529	putative tumor suppressor
41114_at	up	0.009572837	microtubule associated testis specific serine/threonine protein kinase
39635_at	up	0.009598631	KIAA0960 protein
867_s_at	up	0.009646891	thrombospondin 1
1289_at	up	0.009657092	glutathione S-transferase M5
39132_at	down	0.009658304	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
31980_at	up	0.009659298	winged-helix nude
33075_at	up	0.009675595	p21 (CDKN1A)-activated kinase 3
38448_at	up	0.009681742	actinin, alpha 2
34089_at	up	0.009695291	KIAA1030 protein
31587_at	up	0.009704155	solute carrier family 14 (urea transporter), member 2
31390_at	up	0.00970876	zinc finger protein 154 (pHZ-92)
31644_at	up	0.009719178	chemokine (C-C motif) ligand 27
1760_s_at	up	0.009726568	protein tyrosine phosphatase, non-receptor type 7
40491_at	up	0.009743005	retinoblastoma binding protein 1-like 1
36815_at	up	0.009778133	
33969_at	up	0.009780589	interferon, omega 1
32784_at	down	0.009784866	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
40861_at	down	0.009811631	mortality factor 4 like 2
39473_r_at	up	0.0099094	protein tyrosine phosphatase type IVA, member 3
40058_s_at	up	0.009913258	LIM protein (similar to rat protein kinase C-binding enigma)
1722_at	up	0.009928793	mitogen-activated protein kinase kinase 5
41074_at	up	0.009948477	G protein-coupled receptor 49
1488_at	up	0.009953543	protein tyrosine phosphatase, receptor type, K
38850_at	up	0.009961288	
1746_s_at	up	0.009966628	
39059_at	up	0.009967884	7-dehydrocholesterol reductase
40252_g_at	up	0.009972964	HIV-1 rev binding protein 2
35695_at	down	0.009979132	Chediak-Higashi syndrome 1

34952_at	up	0.010018587	Dombrock blood group
38734_at	up	0.010025605	phospholamban
36737_at	up	0.010027033	crystallin, beta A4
41025_r_at	up	0.010038866	glycophorin E
36020_at	up	0.010041904	KIAA1641 protein
39281_at	up	0.010049567	Rho guanine nucleotide exchange factor (GEF) 11
31931_f_at	up	0.010060411	Rhesus blood group, CcEe antigens
380_at	up	0.010096649	T-box 5
31471_at	up	0.010173071	
32699_s_at	up	0.010181466	poliovirus receptor
36869_at	up	0.010188243	paired box gene 8
1241_at	down	0.010202166	protein tyrosine phosphatase type IVA, member 2
833_at	up	0.010217675	integrin, alpha X (antigen CD11C (p150), alpha polypeptide)
1296_at	up	0.01026762	cadherin 15, M-cadherin (myotubule)
40142_at	up	0.010274697	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24
41783_at	up	0.010279779	cellular retinoic acid binding protein 2
40294_at	up	0.010290318	ATP-binding cassette, sub-family B (MDR/TAP), member 9
38170_at	up	0.010301634	
36398_at	up	0.010305459	RNA, U2 small nuclear
41127_at	up	0.010310422	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4
41445_at	up	0.010315079	transforming growth factor, beta 1 (Camurati-Engelmann disease)
37184_at	up	0.010336804	syntaxin 1A (brain)
37515_at	up	0.010347685	mannan-binding lectin serine protease 2
39640_at	up	0.010360104	glutamine-fructose-6-phosphate transaminase 2
33823_at	up	0.010369528	scavenger receptor class B, member 2
34448_s_at	up	0.010370222	caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2)
36774_f_at	up	0.01037535	proline-rich protein BstNI subfamily 1
35764_at	down	0.0104032	oral-facial-digital syndrome 1
35939_s_at	up	0.01040841	POU domain, class 4, transcription factor 1
36807_at	up	0.010412052	TED protein
33034_at	up	0.01042984	rhomboid, veinlet-like 1 (Drosophila)
36660_at	down	0.010439681	RAB11A, member RAS oncogene family

37031_at	down	0.010449766	chromosome 9 open reading frame 10
39165_at	down	0.010454441	nitrogen fixation cluster-like
32339_at	up	0.010466418	pancreatic polypeptide
540_at	up	0.010490446	heat shock 27kDa protein 2
31671_at	down	0.010490552	RNA binding motif, single stranded interacting protein 1
40792_s_at	up	0.010508924	triple functional domain (PTPRF interacting)
31423_at	up	0.010540363	
34786_at	down	0.010555311	jumonji domain containing 1
32217_at	down	0.010581595	chromosome 12 open reading frame 22
41290_at	up	0.010587378	neural cell adhesion molecule 1
33470_at	up	0.010596187	KIAA1719 protein
39229_at	up	0.010609138	serologically defined colon cancer antigen 1
38209_at	up	0.010647629	prostaglandin E receptor 1 (subtype EP1), 42kDa
1138_at	up	0.010681017	solute carrier family 20 (phosphate transporter), member 1
41351_at	up	0.010681598	collagen, type VI, alpha 1
38530_at	up	0.010725893	hypothetical protein FLJ22709
32815_at	up	0.010728637	
41223_at	down	0.010758437	cytochrome c oxidase subunit Va
39448_r_at	up	0.010786654	B7 gene
38208_at	up	0.010791254	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3
33902_at	up	0.010802466	glycerol-3-phosphate dehydrogenase 1 (soluble)
32885_f_at	up	0.010812006	proline-rich protein BstNI subfamily 2
41253_s_at	down	0.010819631	chorionic somatomammotropin hormone 2
32031_at	up	0.010819727	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
38025_r_at	up	0.010821372	rap2 interacting protein x
35510_at	up	0.010831878	sodium channel, voltage gated, type VIII, alpha
32956_at	up	0.010838375	G protein-coupled receptor, family C, group 5, member B
41033_at	down	0.01084462	zinc finger protein 84 (HPF2)
33768_at	up	0.010848796	dystrophia myotonica-containing WD repeat motif
34449_at	up	0.010856436	caspase 2, apoptosis-related cysteine protease (neural precursor cell expressed, developmentally down-regulated 2)

31674_s_at	up	0.010905397	bromodomain containing 3
32856_at	up	0.010925156	KIAA0819 protein
1401_g_at	up	0.010933721	colony stimulating factor 2 (granulocyte-macrophage)
35147_at	up	0.010946156	MCF.2 cell line derived transforming sequence-like
924_s_at	down	0.010998105	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
40912_s_at	up	0.01100562	biphenyl hydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen)
31457_at	up	0.011007906	forkhead box D2
40653_at	up	0.011010145	regulator of G-protein signalling 7
35815_at	down	0.011012092	huntingtin interacting protein B
33690_at	up	0.011014125	
32271_at	up	0.011029711	FOS-like antigen 1
35164_at	up	0.011029719	Wolfram syndrome 1 (wolframin)
868_at	down	0.011059405	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa
31949_at	up	0.011111935	Ras protein-specific guanine nucleotide-releasing factor 1
34485_r_at	up	0.011126448	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
40189_at	down	0.011156147	SET translocation (myeloid leukemia-associated)
38026_at	up	0.011184842	fibulin 1
32789_at	down	0.01118756	nuclear cap binding protein subunit 2, 20kDa
2087_s_at	up	0.011265547	cadherin 11, type 2, OB-cadherin (osteoblast)
477_at	up	0.011266133	interferon regulatory factor 5
1619_g_at	up	0.011283533	cytochrome P450, family 19, subfamily A, polypeptide 1
31368_at	up	0.011303022	zinc finger protein 291
35484_at	up	0.011329287	
37221_at	down	0.0113471	protein kinase, cAMP-dependent, regulatory, type II, beta
38479_at	down	0.011383491	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B
AFFX-YEL024w/RIP1_at	up	0.011438611	
36061_at	up	0.011458942	
1800_g_at	up	0.011481816	excision repair cross-complementing rodent repair deficiency, complementation group 4
36052_at	up	0.011487914	adducin 2 (beta)
36201_at	up	0.011488798	glyoxalase I
40032_at	up	0.011543083	KIAA0133 gene product



33539_at	up	0.011546061	myelin expression factor 2
35860_r_at	up	0.011555174	
36601_at	down	0.011556615	vinculin
34901_at	up	0.011562757	ubiquitin specific protease 2
31856_at	up	0.011566968	glycoprotein A repetitions predominant
39376_at	down	0.01157243	homeodomain interacting protein kinase 1
37860_at	up	0.011582858	zinc finger protein 337
AFFX-BioDn-5_at	up	0.011589001	
34084_at	up	0.011592343	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)
32880_at	up	0.01161328	secretoglobin, family 1D, member 2
160038_s_at	up	0.011619181	insulin
37007_at	down	0.011628359	tumor differentially expressed 1
36747_at	up	0.011652598	
38882_r_at	up	0.011660597	tripartite motif-containing 16
41724_at	down	0.011675116	accessory protein BAP31
34042_at	up	0.011693218	chondroadherin
37088_at	up	0.011693649	serine/threonine kinase 13 (aurora/IPL1-like)
36452_at	up	0.011707524	synaptopodin
39290_f_at	up	0.011738795	PAI-1 mRNA-binding protein
853_at	down	0.011747537	nuclear factor (erythroid-derived 2)-like 2
36332_at	up	0.011793078	arylalkylamine N-acetyltransferase
32415_at	up	0.011799437	interferon, alpha 5
35659_at	down	0.011837246	interleukin 10 receptor, alpha
38126_at	up	0.011859592	biglycan
37475_at	up	0.011876768	DKFZP434J046 protein
40468_at	down	0.011880956	formin binding protein 1
1218_at	up	0.011899656	nuclear receptor subfamily 2, group F, member 6
34644_at	up	0.011971442	beta-2-microglobulin
40036_at	down	0.011989436	mago-nashi homolog, proliferation-associated (Drosophila)
33922_at	up	0.012007232	PR domain containing 2, with ZNF domain
34803_at	up	0.012039368	ubiquitin specific protease 12
1235_at	down	0.012045788	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
40736_at	up	0.012066991	cadherin 17, LI cadherin (liver-intestine)

36967_g_at	up	0.012072207	ankyrin 3, node of Ranvier (ankyrin G)
36829_at	up	0.01208281	period homolog 1 (Drosophila)
41802_at	up	0.012147295	hypothetical protein FLJ22531
34307_at	down	0.012151793	transmembrane 9 superfamily member 2
1631_at	up	0.012168955	
40385_at	up	0.012170497	chemokine (C-C motif) ligand 20
31694_at	up	0.012212301	regulatory solute carrier protein, family 1, member 1
40299_at	up	0.012242936	G-protein coupled receptor
35169_at	up	0.01227325	collagen, type XVI, alpha 1
31474_r_at	down	0.012310633	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
36557_at	up	0.012312191	calcium channel, voltage-dependent, beta 1 subunit
37147_at	up	0.012334348	stem cell growth factor; lymphocyte secreted C-type lectin
36544_at	up	0.012341199	
40604_at	down	0.012357898	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
37746_r_at	up	0.012358556	suppression of tumorigenicity 5
41101_at	up	0.012390473	Sac domain-containing inositol phosphatase 3
37310_at	up	0.01240215	plasminogen activator, urokinase
32232_at	down	0.012415251	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa
AFFX-BioC-5_at	up	0.012424633	
32101_at	up	0.01242678	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)
32079_at	up	0.012428316	kinesin family member 13B
38710_at	up	0.01246202	ubiquitin-specific protease otubain 1
40961_at	down	0.012462865	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
32192_g_at	up	0.012473564	ring finger protein 110
38441_s_at	down	0.012487948	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)
36016_at	up	0.012489251	cortistatin
41305_at	up	0.01250619	solute carrier family 5 (sodium/glucose cotransporter), member 2
41289_at	up	0.012530504	neural cell adhesion molecule 1
32613_at	up	0.012539347	synaptic vesicle glycoprotein 2B
31734_at	up	0.012541867	homeo box C11
35163_at	down	0.012560197	KIAA1041 protein

41759_at	down	0.012605139	transcription elongation factor B (SIII), polypeptide 1 pseudogene
37561_at	down	0.012613195	nuclear transcription factor Y, alpha
39627_at	up	0.012650879	early endosome antigen 1, 162kD
38413_at	down	0.012716582	defender against cell death 1
35473_at	up	0.012718357	collagen, type I, alpha 1
33724_at	up	0.012747577	breast cancer 1, early onset
572_at	up	0.01277828	TTK protein kinase
33937_at	up	0.012832989	
35229_at	up	0.012850884	carnitine palmitoyltransferase 1A (liver)
39780_at	down	0.01285708	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
41098_at	up	0.012886931	dishevelled associated activator of morphogenesis 2
38128_at	up	0.012911811	N-acetyltransferase 8 (camello like)
35911_r_at	up	0.012913888	matrix metalloproteinase-like 1
34870_at	up	0.012919562	LIM domain binding 3
31705_at	up	0.012932212	ARS component B
32469_at	down	0.012937069	carcinoembryonic antigen-related cell adhesion molecule 3
33808_at	up	0.012942298	TEA domain family member 3
36652_at	up	0.012968039	uroporphyrinogen III synthase (congenital erythropoietic porphyria)
35172_at	down	0.012992358	tyrosylprotein sulfotransferase 2
40186_at	up	0.013034664	dual specificity phosphatase 9
39454_f_at	up	0.013098402	T-cell leukemia, homeobox 2
36922_at	up	0.013121302	ribonucleotide reductase M2 polypeptide
39840_at	up	0.013143318	cysteine knot superfamily 1, BMP antagonist 1
39031_at	up	0.013178811	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
1032_at	up	0.013182233	dihydropyrimidine dehydrogenase
37314_at	up	0.013203795	chromosome 14 open reading frame 11
36814_at	down	0.013248989	hypothetical protein KIAA1109
31434_at	up	0.013251593	
1523_g_at	up	0.013266534	tyrosine kinase, non-receptor, 1
210_at	up	0.013282218	phospholipase C, beta 2
31450_s_at	up	0.013347747	Ras-like without CAAX 2
35303_at	down	0.013354891	insulin induced gene 1
37042_at	up	0.013358442	hyaluronoglucosaminidase 2
37675_at	down	0.013393808	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3

40363_r_at	up	0.013426669	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
745_at	up	0.013436936	transcription elongation factor A (SII), 2
39427_at	down	0.013456646	ubiquinol-cytochrome c reductase binding protein
33267_at	down	0.013514384	
32381_at	up	0.013553578	RAR-related orphan receptor B
31626_i_at	up	0.013564285	amine oxidase pseudogene
39469_s_at	up	0.013613609	ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2
1950_s_at	up	0.013677073	MAD, mothers against decapentaplegic homolog 3 (Drosophila)
40512_at	up	0.01367746	chimerin (chimaerin) 1
37729_at	down	0.013682129	exportin 1 (CRM1 homolog, yeast)
40402_at	up	0.013695808	solute carrier family 6 (neurotransmitter transporter, noradrenalin) member 2
40595_at	up	0.01373059	Treacher Collins-Franceschetti syndrome 1
37756_at	up	0.01375692	RYK receptor-like tyrosine kinase
1664_at	up	0.01381471	
31636_s_at	up	0.013826343	solute carrier family 18 (vesicular acetylcholine), member 3
41293_at	up	0.013828112	keratin 7
33546_at	up	0.013836831	
31386_at	up	0.013843476	immunoglobulin kappa variable 1/OR15-118
33495_at	up	0.013909579	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2
37274_at	up	0.013914109	biotinidase
41488_at	down	0.013928912	hypothetical protein A-211C6.1
31999_at	up	0.013935691	ATP-binding cassette, sub-family A (ABC1), member 1
39360_at	down	0.013945505	sorting nexin 3
34791_at	down	0.013953726	t-complex 1
34324_at	down	0.01395827	ceroid-lipofuscinosis, neuronal 5
40819_at	up	0.013958858	RNA binding motif protein 8A
41529_g_at	down	0.013984956	
35793_at	down	0.014000217	Ras-GTPase activating protein SH3 domain-binding protein 2
36075_at	up	0.014076733	RAB, member of RAS oncogene family-like 4
33322_i_at	up	0.014082655	stratifin

35978_at	up	0.014105216	proline-rich Gla (G-carboxyglutamic acid) polypeptide 1
37961_at	up	0.014113688	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma)
35521_at	up	0.01411609	claudin 9
33266_at	up	0.014136389	serine/threonine kinase 12
31325_at	up	0.014137098	
41001_at	up	0.014148684	likely ortholog of mouse rabphilin 3A
41123_s_at	up	0.014166567	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)
41079_at	up	0.014179586	amiloride-sensitive cation channel 3, testis
33221_at	up	0.014203535	PAX transcription activation domain interacting protein 1 like
806_at	up	0.014209175	cytokine-inducible kinase
39657_at	up	0.014284559	keratin 4
36625_at	up	0.014320189	peroxisomal long-chain acyl-coA thioesterase
38538_at	up	0.014353625	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1
37189_at	up	0.014377897	phosphomannomutase 1
33670_at	up	0.014395478	
41602_at	up	0.014427132	hippocalcin
39490_f_at	up	0.014434597	ADP-ribosylation factor GTPase activating protein 3
39137_at	up	0.014438261	nuclear factor related to kappa B binding protein
32104_i_at	up	0.014440307	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
37976_at	up	0.014454216	Ig superfamily protein
36420_at	up	0.014470534	intersectin 2
37204_at	up	0.014470631	pre-alpha (globulin) inhibitor, H3 polypeptide
742_at	up	0.014501825	hyaluronan binding protein 2
277_at	down	0.014527659	myeloid cell leukemia sequence 1 (BCL2-related)
40945_at	up	0.014552217	TGFB inducible early growth response 2
31833_at	up	0.014573625	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha
36913_at	down	0.014582499	stem-loop (histone) binding protein
33783_at	up	0.014601433	plexin B1
34764_at	up	0.014611105	leucyl-tRNA synthetase, mitochondrial
32269_at	up	0.014621549	BAI1-associated protein 1
912_s_at	up	0.014641028	phospholipase A2, group IB (pancreas)
37227_at	up	0.014654821	apoptotic protease activating factor

33440_at	down	0.014672964	transcription factor 8 (represses interleukin 2 expression)
38943_at	down	0.014708654	holocytochrome c synthase (cytochrome c heme-lyase)
35113_at	up	0.014808127	solute carrier family 22 (organic cation transporter), member 1
38181_at	up	0.014820162	matrix metalloproteinase 11 (stromelysin 3)
41018_at	up	0.014823451	DKFZP564O243 protein
35266_at	down	0.014833914	bladder cancer associated protein
463_g_at	up	0.014919402	nuclear factor I/B
33545_at	up	0.014947629	sodium channel, voltage-gated, type IV, alpha
41785_at	down	0.014955497	eukaryotic translation initiation factor 4 gamma, 2
37905_r_at	up	0.015015551	
39564_s_at	up	0.015051374	ATP-binding cassette, sub-family B (MDR/TAP), member 6
35342_at	down	0.015052012	
36378_at	up	0.015073855	uroplakin 1A
35434_at	up	0.015123449	MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D)
41525_at	up	0.015136461	high-mobility group 20B
37276_at	down	0.015149254	IQ motif containing GTPase activating protein 2
1424_s_at	down	0.015163256	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
37442_at	down	0.015178917	hypothetical protein DKFZp586l1420
39214_at	up	0.015195618	plexin B3
36720_at	up	0.015223928	pyruvate dehydrogenase kinase, isoenzyme 3
40941_at	up	0.015261702	VAMP (vesicle-associated membrane protein)-associated protein B and C
33374_at	up	0.015278411	complement component 2
40027_at	down	0.015289109	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit s (factor B)
31738_at	up	0.015316801	
33642_s_at	up	0.015319584	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
34525_at	up	0.015328652	T-cell leukemia/lymphoma 1B
34923_at	up	0.015331205	KIAA0522 protein
36718_s_at	down	0.015337288	pyruvate dehydrogenase kinase, isoenzyme 3
33666_at	down	0.015344184	heterogeneous nuclear ribonucleoprotein C (C1/C2)

39383_at	up	0.015367512	adenylate cyclase 6
37248_at	up	0.015368335	carboxypeptidase Z
33807_at	up	0.015395268	phosphoinositol 3-phosphate-binding protein-3
1971_g_at	up	0.015433856	fragile histidine triad gene
32522_f_at	up	0.015452907	clathrin, light polypeptide (Lcb)
40237_at	up	0.015487652	tumor suppressing subtransferable candidate 3
35295_g_at	down	0.01549105	Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro)
218_at	down	0.015538652	IK cytokine, down-regulator of HLA II
39639_s_at	up	0.015540109	transition protein 1 (during histone to protamine replacement)
33144_at	up	0.015542466	solute carrier family 16 (monocarboxylic acid transporters), member 3
34697_at	up	0.015588844	low density lipoprotein receptor-related protein 6
39868_at	up	0.015598787	poly(rC) binding protein 3
35091_at	up	0.015609298	neuregulin 2
1096_g_at	up	0.015618275	CD19 antigen
31452_at	up	0.015629582	survival motor neuron pseudogene
39511_at	up	0.015634398	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4
36826_at	up	0.015634839	general transcription factor IIF, polypeptide 1, 74kDa
1415_at	up	0.015636698	embryonal Fyn-associated substrate
41279_f_at	up	0.015657636	mitogen-activated protein kinase 8 interacting protein 1
36326_at	up	0.015683908	nescient helix loop helix 2
1555_f_at	up	0.015707626	cytochrome P450, family 2, subfamily A, polypeptide 7
37133_at	up	0.015716843	serine/threonine kinase 23
33610_at	up	0.015729266	claudin 8
40674_s_at	up	0.015769271	homeo box C6
39765_at	up	0.015769941	talin 2
35352_at	up	0.015775962	aryl-hydrocarbon receptor nuclear translocator 2
35974_at	down	0.015787229	lymphoid-restricted membrane protein
34802_at	up	0.015795589	collagen, type VI, alpha 2
34902_at	up	0.015815292	KIAA0492 protein
984_g_at	up	0.015817247	mitogen-activated protein kinase 12
37267_at	up	0.015828594	thimet oligopeptidase 1

34002_at	up	0.0158432	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2
38946_at	up	0.015843586	protein phosphatase, EF hand calcium-binding domain 1
31704_at	up	0.015883818	deoxyribonuclease I-like 2
41042_r_at	up	0.01592032	myosin VIIA (Usher syndrome 1B (autosomal recessive, severe))
31926_at	up	0.01593408	cytochrome P450, family 7, subfamily A, polypeptide 1
37158_at	up	0.015948773	ATP-binding cassette, sub-family C (CFTR/MRP), member 1
1896_s_at	up	0.015958981	
41416_at	up	0.015961067	fibrinogen-like 1
35910_f_at	up	0.015964906	matrix metalloproteinase-like 1
38582_at	up	0.015969003	serine protease inhibitor, Kazal type 1
38114_at	down	0.016076891	RAD21 homolog (S. pombe)
40926_at	up	0.016084766	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
34394_at	down	0.01609586	activity-dependent neuroprotector
31556_at	up	0.016136864	serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2
32103_at	up	0.016177838	
38572_at	up	0.016177861	FGFR1 oncogene partner
34864_at	up	0.016199781	hypothetical protein CGI-57
35095_r_at	down	0.016220568	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3
1391_s_at	up	0.016223701	cytochrome P450, family 4, subfamily A, polypeptide 11
31902_at	up	0.016232561	deiodinase, iodothyronine, type II
37303_at	down	0.016339359	ADP-ribosyltransferase (NAD <sup>+</sup> ; poly (ADP-ribose) polymerase)-like 1
38841_at	down	0.016345714	putative glioblastoma cell differentiation-related
32204_at	up	0.016360734	phosphodiesterase 6G, cGMP-specific, rod, gamma
37060_at	up	0.016378817	collagen, type XIX, alpha 1 insulin receptor substrate 2 serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)
31577_at	up	0.016382282	
40180_at	up	0.016385547	
39775_at	up	0.016407009	
41143_at	down	0.016409508	calmodulin 1 (phosphorylase kinase, delta)
36583_at	down	0.016418131	sorting nexin 1
35828_at	up	0.016423982	cysteine-rich protein 2



37573_at	up	0.016431244	angiopoietin-like 2
39784_at	down	0.016449639	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
40745_at	up	0.016531089	adaptor-related protein complex 1, beta 1 subunit
36987_at	up	0.016535539	lamin B2
35565_at	up	0.016616751	LanC lantibiotic synthetase component C-like 2 (bacterial)
37672_at	down	0.016674897	ubiquitin specific protease 7 (herpes virus-associated)
39103_s_at	up	0.016676884	
37554_at	up	0.016679024	kallikrein 6 (neurosin, zyme)
38657_s_at	up	0.016700888	clathrin, light polypeptide (Lca)
36019_at	up	0.016718156	serine/threonine kinase 19
34214_at	up	0.016732911	KIAA0644 gene product
36844_at	up	0.016756145	dedicator of cyto-kinesis 3
41711_at	up	0.016773547	thioredoxin reductase 2
939_at	up	0.016782506	
35396_at	up	0.016794613	hyaluronan synthase 2
35198_at	up	0.016796595	promethin
33947_at	up	0.016809014	G protein-coupled receptor 3
38840_s_at	down	0.01682395	profilin 2
31890_s_at	down	0.016843461	zinc finger protein 143 (clone pHZ-1)
34024_at	up	0.016873841	chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease)
37146_at	down	0.016887348	KIAA0404 protein
39801_at	up	0.01689521	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
40879_at	down	0.016929255	coiled-coil protein BICD2
33595_r_at	up	0.016932374	recombination activating gene 2
706_at	down	0.016934279	
35798_at	up	0.01694392	NS1-associated protein 1
1713_s_at	down	0.016952268	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
35112_at	up	0.016979898	regulator of G-protein signalling 9
32163_f_at	up	0.016998487	chorionic somatomammotropin hormone 2
31881_at	down	0.017004901	mob protein
31775_at	up	0.017053345	surfactant, pulmonary-associated protein D
37995_s_at	down	0.017056726	fragile X mental retardation 1
35915_at	up	0.017078706	inhibin, beta C
36896_s_at	down	0.017114074	aryl hydrocarbon receptor nuclear translocator-like
34222_at	up	0.017137337	hypothetical protein from clone 24828

39194_at	up	0.017213039	glutathione peroxidase 2 (gastrointestinal)
33879_at	up	0.017232449	type I sigma receptor
36152_at	up	0.017242899	GDP dissociation inhibitor 1
263_g_at	down	0.017262681	adenosylmethionine decarboxylase 1
36690_at	down	0.017262777	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
35398_at	up	0.017273339	
38046_at	down	0.017297027	IK cytokine, down-regulator of HLA II
1483_at	up	0.017308878	cadherin 4, type 1, R-cadherin (retinal)
34567_at	up	0.017357311	cylicin, basic protein of sperm head cytoskeleton 2
33122_at	up	0.017373574	regulator of G-protein signalling 10
884_at	up	0.017392757	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
35080_at	up	0.017429659	neurotensin receptor 1 (high affinity)
2022_at	up	0.017431884	v-akt murine thymoma viral oncogene homolog 2
40535_i_at	up	0.017441987	translation initiation factor IF2
32587_at	down	0.017445795	zinc finger protein 36, C3H type-like 2
1399_at	down	0.017450684	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)
1169_at	up	0.017478787	protocadherin gamma subfamily B, 7
41285_at	up	0.017525434	inositol polyphosphate-5-phosphatase, 40kDa
37228_at	up	0.017538384	polo-like kinase (Drosophila)
35876_s_at	up	0.017574915	sphingosine-1-phosphate lyase 1
32903_at	up	0.017581104	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)
35180_at	down	0.017588189	c-Mpl binding protein
1051_g_at	up	0.017597054	melan-A
33126_at	down	0.017609759	glycosyltransferase AD-017
33436_at	up	0.017614337	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)
33806_at	up	0.01762397	hypothetical protein FLJ22195
39965_at	up	0.01764993	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)
385_at	up	0.017687295	
40959_at	up	0.017704581	KIAA0599 protein
36356_at	up	0.017780577	growth differentiation factor 5 (cartilage-derived morphogenetic protein-1)

39855_at	up	0.017795155	Fzr1 protein
40931_at	down	0.017817731	CGI-100 protein
492_g_at	up	0.017826554	protein tyrosine phosphatase, receptor type, G
1420_s_at	down	0.017834415	eukaryotic translation initiation factor 4A, isoform 2
36407_at	up	0.017841019	kallikrein 13
37185_at	up	0.017841095	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2
40872_at	down	0.017872198	cytochrome c oxidase subunit VIb
37334_at	down	0.017882062	heterogeneous nuclear ribonucleoprotein A0
39185_at	down	0.017885168	hypothetical protein 628
37766_s_at	down	0.017887937	proteasome (prosome, macropain) 26S subunit, ATPase, 5
32005_at	up	0.017891687	pro-melanin-concentrating hormone
31688_at	up	0.017957105	skin-specific protein
2055_s_at	up	0.01796478	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
35214_at	up	0.018093625	UDP-glucose dehydrogenase
34161_at	up	0.018130162	lactoperoxidase
36392_at	up	0.018158369	zinc finger protein 135 (clone pHZ-17)
33310_at	down	0.018160642	comparative gene identification 58
38298_at	up	0.018174474	potassium large conductance calcium-activated channel, subfamily M, beta member 1
39200_s_at	up	0.018250192	growth differentiation factor 11
625_at	up	0.018283211	vesicle amine transport protein 1 homolog (T californica)
36834_at	up	0.018291464	DKFZP564G202 protein
40950_at	up	0.018330724	dynein, cytoplasmic, light intermediate polypeptide 2
35790_at	down	0.018330827	vacuolar protein sorting 26 (yeast)
38915_at	up	0.018336984	KIAA0563 gene product
41394_at	up	0.018360549	phospholipase D2
33961_at	up	0.018361619	
37602_at	up	0.018387236	guanidinoacetate N-methyltransferase
507_s_at	down	0.018388413	E74-like factor 2 (ets domain transcription factor)
31637_s_at	up	0.018396658	nuclear receptor subfamily 1, group D, member 1
36797_at	up	0.018409859	sialophorin (gpL115, leukosialin, CD43)
39345_at	down	0.018412516	Niemann-Pick disease, type C2
40188_f_at	up	0.018416817	
38374_at	down	0.018474391	TGFB inducible early growth response

38104_at	down	0.018535035	2,4-dienoyl CoA reductase 1, mitochondrial
35354_at	up	0.018538623	synaptogyrin 1
34336_at	down	0.018562306	lysyl-tRNA synthetase
38526_at	up	0.01860093	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 duncce homolog, Drosophila)
36032_at	down	0.018630726	HSPCO34 protein
35485_at	up	0.01866013	glutamate receptor, metabotropic 4
39547_at	up	0.018672308	RAN binding protein 9
37875_at	up	0.018679056	glycoprotein A33 (transmembrane)
730_r_at	up	0.018699817	
33985_s_at	up	0.018705931	heat shock 90kDa protein 1, beta
39319_at	down	0.018716388	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)
40094_r_at	up	0.018725325	Lutheran blood group (Auberger b antigen included)
36924_r_at	up	0.018756701	secretogranin II (chromogranin C)
36306_at	up	0.018756705	potassium voltage-gated channel, KQT-like subfamily, member 3
1704_at	up	0.018767596	vav 2 oncogene
41399_at	down	0.018773794	KIAA1111 protein
40804_at	up	0.01880313	nucleoporin 88kDa
31837_at	up	0.018865712	hypothetical protein BC002942
35725_at	down	0.018871291	karyopherin alpha 3 (importin alpha 4)
38154_at	up	0.018880449	
39140_at	down	0.018895051	nucleic acid helicase DDXx
34055_at	up	0.018918709	activin A receptor, type IB
41804_at	up	0.018951167	hypothetical protein FLJ22531
31701_r_at	up	0.018965341	B1 for mucin
32909_at	up	0.019004154	aquaporin 5
32399_at	up	0.019021041	ecotropic viral integration site 1
40496_at	up	0.01903891	complement component 1, s subcomponent
36330_at	up	0.019050873	cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotransferase)
888_s_at	up	0.019070811	LAG1 longevity assurance homolog 1 (S. cerevisiae)
37748_at	down	0.019075149	KIAA0232 gene product
41418_at	up	0.019075413	latrophilin 1
40488_at	up	0.019080462	dystrophin (muscular dystrophy, Duchenne and Becker types)
40390_at	up	0.01908294	serine dehydratase
41078_at	up	0.019088607	KIAA0150 protein
38626_at	down	0.019091364	KIAA0399 protein

650_s_at	down	0.019102817	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma
39245_at	up	0.019111468	
36080_at	up	0.0191278	clock homolog (mouse)
39408_at	up	0.019130961	hypothetical protein MGC5139
39872_at	up	0.019146391	G-2 and S-phase expressed 1
36119_at	up	0.019160158	caveolin 1, caveolae protein, 22kDa
36570_at	up	0.019170443	calbindin 1, 28kDa
40063_at	down	0.01917505	nuclear domain 10 protein
39113_at	up	0.019182305	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)
36663_at	up	0.019184809	natriuretic peptide precursor A
34573_at	up	0.019216743	ephrin-A3
37615_at	up	0.019228832	growth factor receptor-bound protein 10
34306_at	down	0.019238039	muscleblind-like (Drosophila)
40344_at	up	0.019239373	neuroligin 1
36375_at	up	0.019280928	outer dense fiber of sperm tails 1
32975_g_at	up	0.01928292	homolog of Yeast RRP4 (ribosomal RNA processing 4), 3'-5'-exoribonuclease
692_s_at	up	0.01928419	superoxide dismutase 3, extracellular
38088_r_at	up	0.019334463	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)
36139_at	up	0.01937145	chromosome 6 open reading frame 4
33329_at	up	0.019378158	nuclear factor I/C (CCAAT-binding transcription factor)
35598_at	up	0.019416892	histone 1, H3e
35821_at	down	0.019431843	histone deacetylase 3
41241_at	down	0.019435076	asparaginyl-tRNA synthetase
667_at	up	0.019461528	arginine vasopressin receptor 2 (nephrogenic diabetes insipidus)
39809_at	down	0.019462445	HMG-box containing protein 1
34851_at	up	0.019463854	serine/threonine kinase 6
1007_s_at	up	0.0194894	discoidin domain receptor family, member 1
567_s_at	up	0.01953774	promyelocytic leukemia
40355_at	up	0.019595751	AND-1 protein
37562_at	up	0.019609089	protocadherin 1 (cadherin-like 1)
39451_i_at	up	0.019623483	iduronate 2-sulfatase (Hunter syndrome)
32785_at	down	0.019631759	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa
694_at	up	0.019702348	
36276_at	up	0.019710749	contactin 2 (axonal)
668_s_at	up	0.019731276	matrix metalloproteinase 7 (matrilysin, uterine)

31468_f_at	up	0.019744635	glutamate receptor, metabotropic 1
40418_at	down	0.019762763	retinoblastoma binding protein 4
36051_s_at	up	0.01982094	adducin 2 (beta)
34667_at	up	0.019830749	nuclear transcription factor, X-box binding 1
37565_at	down	0.019838268	monocyte to macrophage differentiation-associated
36954_at	down	0.019858282	KIAA0218 gene product
31746_at	up	0.019892901	zinc finger protein 204
1481_at	up	0.019894049	matrix metalloproteinase 12 (macrophage elastase)
666_at	up	0.019910172	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 duncce homolog, Drosophila)
1141_at	up	0.019912154	melanocortin 5 receptor
39037_at	down	0.019935896	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2
33673_r_at	up	0.019947098	UDP glycosyltransferase 2 family, polypeptide B17
33652_at	up	0.019972991	a disintegrin and metalloproteinase domain 20
35534_at	up	0.020002103	KIAA0514 gene product
34824_at	down	0.020009104	ubiquitin 2
39108_at	up	0.020020999	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
31810_g_at	up	0.020025692	contactin 1
32595_at	down	0.02002983	G-rich RNA sequence binding factor 1
33345_at	up	0.020031007	kinesin family member 3C
39294_at	up	0.020106081	nuclear receptor subfamily 2, group F, member 1
1834_at	up	0.02010754	putative G protein coupled receptor
33622_at	up	0.020119043	calcium channel, voltage-dependent, L type, alpha 1C subunit
40598_at	up	0.020139375	START domain containing 5
34846_at	up	0.020142879	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta
32928_at	up	0.020150947	POU domain, class 2, transcription factor 3
37073_at	up	0.020168835	eyes absent homolog 1 (Drosophila)
41784_at	down	0.020217509	SR rich protein
34184_at	up	0.020259648	adenomatous polyposis coli like
38477_at	down	0.020271492	diphtheria toxin resistance protein required for diphthamide biosynthesis-like 1 (S. cerevisiae)
40260_g_at	up	0.020317242	RNA binding motif protein 9
40740_at	up	0.020333636	paired box gene 6 (aniridia, keratitis)

36007_at	up	0.020396168	DKFZP586L151 protein
36380_at	up	0.020398685	DKFZP434F122 protein
41574_at	down	0.020400712	pinin, desmosome associated protein
39879_s_at	up	0.020473075	hypothetical protein FLJ10120
33787_at	up	0.020483026	KIAA0537 gene product
33008_at	up	0.020521776	olfactory receptor, family 7, subfamily E, member 24 pseudogene
33294_at	down	0.020522678	KIAA0116 protein
33241_at	down	0.020533956	KIAA0626 gene product
35584_s_at	up	0.020544608	calcium channel, voltage-dependent, alpha 1F subunit
36355_at	up	0.02055766	involucrin
33681_at	up	0.020563179	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
33558_at	up	0.020601885	T-box 5
34778_at	up	0.020605113	
33319_at	down	0.02062051	axin 1
33150_at	down	0.020623787	disrupter of silencing 10
1549_s_at	up	0.02062695	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4
34274_at	down	0.020627926	RNA binding motif protein 16
32637_r_at	up	0.020660502	PI-3-kinase-related kinase SMG-1
37201_at	up	0.020782803	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)
40003_at	up	0.020809717	glycoprotein 2 (zymogen granule membrane)
38605_at	down	0.020824508	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa
36775_f_at	up	0.020845451	proline-rich protein BstNI subfamily 2
1557_at	down	0.020870386	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)
1371_s_at	up	0.02094109	cytochrome P450, family 2, subfamily B, polypeptide 6
504_at	down	0.020955749	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
36074_at	up	0.02103264	imprinted in Prader-Willi syndrome
41335_at	down	0.021053426	DKFZP566O1646 protein
37337_at	down	0.021053683	small nuclear ribonucleoprotein polypeptide G
34381_at	down	0.02108904	cytochrome c oxidase subunit VIIc
36640_at	up	0.021092759	myosin, light polypeptide 2, regulatory, cardiac, slow
36580_at	down	0.02112571	hypothetical protein FLJ13910
34172_s_at	up	0.021127469	DNA segment on chromosome X and Y (unique) 155 expressed sequence

37490_at	up	0.021147824	solute carrier family 4, anion exchanger, member 3
40454_at	up	0.021159268	FAT tumor suppressor homolog 1 (Drosophila)
37541_at	up	0.021166157	selectin P ligand
40261_at	up	0.021175781	RNA binding motif protein 9
32463_at	up	0.021175784	Rho GTPase activating protein 6
38146_at	up	0.021176618	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)
34495_r_at	up	0.021186298	synaptogyrin 4
32850_at	down	0.021186976	nucleoporin 153kDa
38963_i_at	up	0.021187774	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
365_at	up	0.021193084	cylicin, basic protein of sperm head cytoskeleton 1
35276_at	up	0.02120371	claudin 4
33875_at	down	0.021227384	ATPase; H+ transporting, lysosomal 9kDa, V0 subunit e
36729_g_at	up	0.02125517	adrenergic, alpha-1D-, receptor
34922_at	up	0.02126488	cadherin 19, type 2
41425_at	down	0.021323848	Friend leukemia virus integration 1
41256_at	down	0.021325224	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
39341_at	up	0.021340838	thyroid hormone receptor interactor 6
40558_at	up	0.021360635	guanylate cyclase activator 1B (retina)
41086_at	up	0.021365747	regulator of G-protein signalling 20
38592_s_at	up	0.021377698	KIAA0284 protein
41347_at	up	0.021382759	iroquois homeobox protein 5
40411_at	down	0.021393313	nuclear receptor coactivator 6
1344_at	up	0.02140639	paired box gene 3 (Waardenburg syndrome 1)
38117_at	up	0.021409201	SEC24 related gene family, member C (S. cerevisiae)
34147_g_at	up	0.021417061	8-oxoguanine DNA glycosylase
33363_at	up	0.021424419	JTV1 gene
39966_at	up	0.021450725	chondroitin sulfate proteoglycan 5 (neuroglycan C)
38499_s_at	up	0.021471019	myelin-associated oligodendrocyte basic protein
39914_r_at	up	0.02147462	transient receptor potential cation channel, subfamily M, member 2
36271_at	up	0.021478981	KIAA1024 protein
40017_at	up	0.021500608	DKFZP586H2123 protein
40141_at	down	0.021547278	cullin 4B
39857_at	down	0.021570023	syntaxin 11



34708_at	up	0.021612712	ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)
40111_g_at	up	0.02161511	isocitrate dehydrogenase 3 (NAD+) beta
38779_r_at	up	0.021635798	hepatoma-derived growth factor (high-mobility group protein 1-like)
41705_at	up	0.021662157	radical fringe homolog (Drosophila)
35533_f_at	up	0.021728712	killer cell lectin-like receptor subfamily C, member 4
34682_at	up	0.021746147	hypothetical protein DKFZp566H0824
40484_g_at	up	0.021753668	transcriptional activator of the c-fos promoter
37600_at	up	0.021776035	extracellular matrix protein 1
41830_at	down	0.021821477	KIAA0494 gene product
32293_at	up	0.021838004	luteinizing hormone/choriogonadotropin receptor
38512_r_at	up	0.02189719	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)
31585_at	up	0.021930368	glutamate receptor, metabotropic 7
38096_f_at	down	0.021970254	major histocompatibility complex, class II, DP beta 1
39792_at	down	0.021996389	heterogeneous nuclear ribonucleoprotein R
33863_at	up	0.022049912	hypoxia up-regulated 1
40596_at	up	0.022092324	Treacher Collins-Franceschetti syndrome 1
32969_r_at	up	0.022103816	VGF nerve growth factor inducible
39803_s_at	up	0.022127147	chromosome 21 open reading frame 2
38229_at	up	0.02213322	cytochrome P450, family 3, subfamily A, polypeptide 5 pseudogene 2
32316_s_at	down	0.022134897	heat shock 90kDa protein 1, alpha
32414_at	up	0.022161556	solute carrier family 28 (sodium-coupled nucleoside transporter), member 1
35037_at	up	0.022179733	
34502_g_at	up	0.022183005	runt-related transcription factor 2
1744_at	up	0.022223723	hepatocyte nuclear factor 4, alpha
36722_s_at	up	0.022234623	
35403_at	down	0.022253864	KIAA1094 protein
41553_at	up	0.022276095	chromosome 8 open reading frame 1
31904_at	up	0.022323192	phosphodiesterase 2A, cGMP-stimulated
1453_at	down	0.022339505	MAD, mothers against decapentaplegic homolog 2 (Drosophila)

271_s_at	up	0.022347943	cathepsin E
35193_at	down	0.022417379	chromosome condensation 1-like
1766_g_at	up	0.022422468	caspase 10, apoptosis-related cysteine protease
1890_at	up	0.022429583	prostate differentiation factor
346_s_at	up	0.022432014	angiotensin II receptor, type 1
36209_at	down	0.022446797	bromodomain containing 2
1271_g_at	up	0.022453783	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)
1608_at	up	0.022472991	
36168_at	up	0.022480506	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
32014_at	up	0.022498779	a disintegrin and metalloproteinase domain 18
161_at	up	0.022524961	RAB9, member RAS oncogene family, pseudogene 1
313_at	up	0.022571235	
37466_at	down	0.022589707	RAB7, member RAS oncogene family-like 1
31521_f_at	down	0.02267027	histone 1, H4j
40378_at	up	0.02267704	SH3-domain GRB2-like 2
160037_at	up	0.022764551	matrix metalloproteinase 15 (membrane-inserted)
31879_at	down	0.022766829	far upstream element (FUSE) binding protein 3
780_at	up	0.022771077	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)
39234_at	up	0.02279868	DKFZP586I111 protein
1675_at	down	0.022841517	RAS p21 protein activator (GTPase activating protein) 1
37328_at	down	0.022861457	pleckstrin
32952_at	up	0.0228892	Retina-derived POU-domain factor-1
34582_at	up	0.022906704	solute carrier family 1 (glial high affinity glutamate transporter), member 2
38224_at	up	0.022931589	small nuclear RNA activating complex, polypeptide 3, 50kDa
32811_at	up	0.022951758	myosin IC
33463_at	up	0.022978048	xanthine dehydrogenase
40830_at	up	0.023005272	DnaJ (Hsp40) homolog, subfamily C, member 4
39913_at	up	0.023012464	heparan sulfate 6-O-sulfotransferase 1

1577_at	up	0.023034692	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
38452_at	up	0.023045399	hypothetical protein MGC5466
37482_at	up	0.023062615	aldo-keto reductase family 1, member B10 (aldose reductase)
33471_g_at	up	0.023074443	KIAA1719 protein
40322_at	up	0.023076512	interleukin 1 receptor-like 1
41871_at	up	0.023125317	lung type-I cell membrane-associated glycoprotein
1598_g_at	up	0.023128654	growth arrest-specific 6
38160_at	down	0.023139429	lymphocyte antigen 75
120_at	up	0.02321075	integrin, alpha 1
32947_at	up	0.023220361	sodium channel, voltage-gated, type IX, alpha
38199_at	up	0.023220366	similar to RIKEN cDNA 2610307I21
32047_at	up	0.023234807	DNA fragmentation factor, 45kDa, alpha polypeptide
32080_at	up	0.023277114	tetracycline transporter-like protein
39483_s_at	down	0.023286561	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
40083_at	down	0.023290559	KIAA0625 protein
39832_at	up	0.023322293	arsenate resistance protein ARS2
1627_at	up	0.02332432	
2032_s_at	up	0.023358429	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
32100_r_at	up	0.023383121	galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)
35644_at	up	0.023398424	hephaestin
38901_at	up	0.023439148	ubiquitin specific protease 19
40183_at	up	0.023444505	coactivator-associated arginine methyltransferase-1
222_at	up	0.023456142	exostoses (multiple) 1
36327_at	up	0.023463563	potassium inwardly-rectifying channel, subfamily J, member 1
32329_at	up	0.023467672	keratin, hair, basic, 6 (monilethrix)
34166_at	up	0.023483105	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7
37690_at	up	0.023498915	ilvB (bacterial acetolactate synthase)-like
40856_at	up	0.023527316	serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1

31740_s_at	up	0.023574982	paired box gene 4
40315_at	up	0.023606902	serine protease inhibitor, Kazal type, 5
40085_s_at	down	0.023614131	transcription factor CP2
32620_at	up	0.023615667	fetuin B
36972_at	down	0.023647274	coated vesicle membrane protein
37784_at	up	0.023651963	
37172_at	up	0.023681682	carboxypeptidase B2 (plasma, carboxypeptidase U)
39412_at	up	0.023685437	tripartite motif-containing 26
33197_at	up	0.023691092	myosin VIIA (Usher syndrome 1B (autosomal recessive, severe))
39876_at	up	0.023730024	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)
1242_at	down	0.023776473	Ets2 repressor factor
40457_at	down	0.023802156	splicing factor, arginine/serine-rich 3
33590_at	up	0.023828936	
40555_at	down	0.023877609	ras homolog gene family, member Q
39706_at	down	0.023892621	copine III
31315_at	up	0.023921194	immunoglobulin lambda locus
39941_at	down	0.023929111	RAD50 homolog (S. cerevisiae)
38649_at	down	0.023932788	KIAA0970 protein
33190_g_at	up	0.023944372	chromosome 10 open reading frame 6
37714_at	up	0.023986452	growth associated protein 43
32243_g_at	up	0.024008044	crystallin, alpha B
41248_at	down	0.024018398	likely ortholog of mouse variant polyadenylation protein CSTF-64
37664_at	up	0.024027194	developmentally regulated GTP binding protein 2
41867_at	up	0.024045128	old astrocyte specifically induced substance
41193_at	down	0.024051364	dual specificity phosphatase 6
35205_at	up	0.02406628	cofactor of BRCA1
40981_at	up	0.024097695	helicase with SNF2 domain 1
38892_at	down	0.024103087	KIAA0240 protein
35363_at	down	0.024128323	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17, 72kDa
36540_at	up	0.024133889	Rho-related BTB domain containing 2
1724_at	up	0.02414433	E2F transcription factor 4, p107/p130-binding
40009_at	up	0.024159688	fragile X mental retardation 2
534_s_at	up	0.02416274	folate receptor 1 (adult)
37723_at	down	0.024176482	cyclin G2
35489_at	up	0.024251424	meprin A, alpha (PABA peptide hydrolase)

227_g_at	down	0.024262631	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
1316_at	up	0.024262768	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)
36018_at	up	0.024269622	SRY (sex determining region Y)-box 10
32728_at	up	0.024280106	amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen)
1825_at	down	0.024316799	IQ motif containing GTPase activating protein 1
38594_i_at	up	0.024320041	KIAA0284 protein
36014_at	up	0.024334234	G protein-coupled receptor 126
1898_at	up	0.024335806	tripartite motif-containing 29
605_at	up	0.024351877	vesicle amine transport protein 1 homolog (T californica)
37122_at	up	0.024415515	perilipin
34933_at	up	0.024433571	paired box gene 9
39897_at	down	0.024487745	splicing factor YT521-B
38558_at	up	0.024488796	myelin associated glycoprotein
1072_g_at	up	0.024497847	GATA binding protein 2
37285_at	up	0.024530431	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)
33069_f_at	up	0.02458139	UDP glycosyltransferase 2 family, polypeptide B15
36031_at	down	0.024608101	inhibitor of growth family, member 1
37511_at	up	0.02461872	B9 protein
39158_at	up	0.024708448	activating transcription factor 5
39744_at	down	0.024753389	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3
1658_g_at	up	0.024762036	protein tyrosine phosphatase, receptor type, R
33346_r_at	up	0.024763958	tubulin, gamma 1
33245_at	down	0.024776732	mitogen-activated protein kinase 13
32066_g_at	up	0.024824897	cAMP responsive element modulator
36143_at	down	0.024857059	caspase 3, apoptosis-related cysteine protease
36269_at	up	0.024858179	a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 3
33071_at	up	0.024871677	histone 1, H2bo
32214_at	down	0.024880537	thioredoxin-like, 32kDa
39797_at	down	0.024903869	ubiquitin ligase E3 alpha-II
33359_at	up	0.024907251	latrophilin 3
34981_at	up	0.024912595	potassium voltage-gated channel, shaker-related subfamily, member 5

41283_at	down	0.02498879	heterogeneous nuclear ribonucleoprotein H3 (2H9)
37134_f_at	up	0.025015777	glutamate receptor, ionotropic, N-methyl D-aspartate 1
35298_at	down	0.02502439	eukaryotic translation initiation factor 3, subunit 7 zeta, 66/67kDa
39625_at	up	0.025069218	acetylcholinesterase (YT blood group)
35387_r_at	up	0.025073822	
31893_at	up	0.025085609	ADP-ribosylation factor-like 2
34305_at	down	0.025125133	poly(rC) binding protein 1
39195_s_at	up	0.025149176	leucine-rich repeats and immunoglobulin-like domains 1
37745_s_at	up	0.025167309	suppression of tumorigenicity 5
39705_at	up	0.025174264	SIN3 homolog B, transcriptional regulator (yeast)
38772_at	up	0.025198255	cysteine-rich, angiogenic inducer, 61
40746_at	up	0.025242905	glutamate receptor, ionotropic, AMPA 2
1482_g_at	up	0.025285618	matrix metalloproteinase 12 (macrophage elastase)
34850_at	down	0.025301859	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)
39123_s_at	up	0.025338973	transient receptor potential cation channel, subfamily C, member
186_at	up	0.025376205	protein kinase, AMP-activated, alpha 2 catalytic subunit
40108_at	down	0.025392776	basic leucine zipper and W2 domains 1
39517_at	down	0.025404739	HTGN29 protein
35997_g_at	up	0.025409702	ZW10 interactor anti-sense
37254_at	up	0.025432778	zinc finger protein 133 (clone pHZ-13)
32872_at	up	0.025443671	YME1-like 1 (S. cerevisiae)
40988_at	down	0.025483862	
35813_at	up	0.025524962	transportin-SR
31778_at	up	0.025549358	gap junction protein, alpha 8, 50kDa (connexin 50)
41652_at	up	0.025591657	collagen, type XI, alpha 2
34805_at	up	0.025620228	hypothetical protein MGC2574
37720_at	down	0.025630855	heat shock 60kDa protein 1 (chaperonin)
35447_s_at	up	0.025651802	acetylserotonin O-methyltransferase
39172_at	down	0.025654012	hypothetical protein FLJ14547
31995_g_at	up	0.025687138	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
36875_at	down	0.02574627	inhibitor of Bruton's tyrosine kinase
32301_at	up	0.025789564	guanylate cyclase 1, soluble, alpha 2
35010_at	up	0.025810869	HLA complex group 8

36367_at	up	0.025830383	protocadherin 11 X-linked
37488_at	up	0.02585489	farnesyltransferase, CAAX box, beta
726_f_at	up	0.025905675	
31935_s_at	up	0.025909825	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, <i>S. cerevisiae</i> )
34819_at	down	0.02591587	CD164 antigen, sialomucin
1449_at	down	0.02591764	proteasome (prosome, macropain) subunit, alpha type, 4
35903_at	up	0.026012105	oligodendrocyte myelin glycoprotein
36890_at	up	0.026034077	periplakin
37794_at	up	0.026039344	
34903_at	up	0.026052906	KIAA1218 protein
38215_at	up	0.026063497	chromosome 22 open reading frame 1
160022_at	down	0.026067385	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog
31727_at	up	0.026069485	ectonucleoside triphosphate diphosphohydrolase 2
33732_at	up	0.026076534	adaptor-related protein complex 4, mu 1 subunit
35845_at	down	0.026142932	SEC24 related gene family, member B ( <i>S. cerevisiae</i> )
1954_at	up	0.026144402	kinase insert domain receptor (a type III receptor tyrosine kinase)
39820_at	up	0.026155871	RNA polymerase I transcription factor RRN3
1772_s_at	down	0.026179299	farnesyltransferase, CAAX box, alpha
34224_at	up	0.026179949	fatty acid desaturase 3
36445_at	up	0.026189391	chemokine (C-C motif) ligand 23
35614_at	down	0.026217146	transcription factor-like 5 (basic helix-loop-helix)
37558_at	up	0.026217683	IGF-II mRNA-binding protein 3
33172_at	up	0.026290468	hypothetical protein FLJ10849
39877_at	up	0.026319532	potassium voltage-gated channel, Shaw-related subfamily, member 4
31922_i_at	up	0.026326432	Ac-like transposable element
40534_at	up	0.026341303	protein tyrosine phosphatase, receptor type, D
1632_at	up	0.026362721	
1411_at	up	0.026495528	cytochrome P450, family 11, subfamily B, polypeptide 1
34576_at	up	0.026513529	melanoma antigen, family A, 8
36037_g_at	up	0.026518478	spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)
37736_at	down	0.02652131	protein-L-isoaspartate (D-aspartate) O-methyltransferase
33898_at	up	0.026563809	microspherule protein 1

1243_at	up	0.026567603	damage-specific DNA binding protein 2, 48kDa
37969_at	up	0.02662293	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
38967_at	down	0.026666699	chromosome 14 open reading frame 2
34563_at	up	0.026707179	kinesin family member 14
41637_at	up	0.026727557	MYLE protein
33887_at	up	0.026739087	hepatocyte growth factor-regulated tyrosine kinase substrate
36568_at	up	0.026745623	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7
37470_at	up	0.026754858	leukocyte-associated Ig-like receptor 1
38076_at	up	0.026783134	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1
598_at	up	0.026832268	collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital)
32540_at	up	0.026889206	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)
34398_at	up	0.026895399	heat shock 105kDa/110kDa protein 1
34880_at	down	0.02690197	hypothetical protein MGC10433
41333_at	down	0.02691227	centaurin, beta 2
687_at	up	0.026947578	
35150_at	up	0.026964489	tumor necrosis factor receptor superfamily, member 5
36736_f_at	down	0.026980201	phosphoserine phosphatase
31716_at	up	0.026993707	protocadherin 1 (cadherin-like 1)
34294_at	up	0.02707396	kinesin family member C3
32898_at	up	0.027097609	actin like protein
40858_at	up	0.02711133	pregnancy specific beta-1-glycoprotein 1
39740_g_at	down	0.02714561	nascent-polypeptide-associated complex alpha polypeptide
32841_at	down	0.027165304	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)
33253_at	down	0.027189829	tripartite motif-containing 14
38680_at	up	0.027225635	small nuclear ribonucleoprotein polypeptide E
40655_at	up	0.027239968	huntingtin-associated protein interacting protein (duo)
1671_s_at	up	0.027242438	mitogen-activated protein kinase 14
335_r_at	up	0.027250575	
31846_at	up	0.02727266	ras homolog gene family, member D



38564_at	up	0.027279452	origin recognition complex, subunit 1-like (yeast)
34926_at	up	0.027289913	CD1A antigen, a polypeptide
39746_at	down	0.027291894	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa
1041_at	up	0.027299453	ephrin-A5
34159_at	up	0.027348803	RAB7, member RAS oncogene family
39972_at	up	0.027368356	G protein-coupled receptor 17
31831_at	up	0.027395463	smoothelin
31800_at	up	0.027462703	
31594_at	up	0.027473933	keratin, hair, acidic, 3A
34154_at	up	0.02749165	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)
38048_at	up	0.027500957	RNA binding protein with multiple splicing
1011_s_at	down	0.027503898	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
35075_at	up	0.027506345	C18B11 homolog (44.9kD)
37374_at	down	0.027538074	annexin A4
33719_at	up	0.027545401	synaptopodin
31446_s_at	up	0.027567801	proline rich 5 (salivary)
34537_at	up	0.027593937	potassium inwardly-rectifying channel, subfamily J, member 12
36274_at	up	0.027615478	solute carrier family 7 (cationic amino acid transporter, y+ system) member 1
36399_at	up	0.027680522	pre-mRNA splicing SR protein rA4
34823_at	down	0.02770756	dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2)
1558_g_at	down	0.027712082	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)
1661_i_at	up	0.027721213	
36715_at	up	0.02776357	adrenergic, alpha-1A-, receptor
39572_at	up	0.027785371	glutamate receptor, ionotropic, kainate 2
38016_at	down	0.027802172	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
38077_at	up	0.027810469	collagen, type VI, alpha 3
40557_at	up	0.02789479	guanylate cyclase activator 1B (retina)
34486_at	up	0.027907141	
39573_at	up	0.027923396	glutamate receptor, ionotropic, kainate 2
37780_at	up	0.027968479	piccolo (presynaptic cytomatrix protein)
32019_at	up	0.02799539	DKFZP434C153 protein

31522_f_at	up	0.028090065	histone 1, H2bf
685_f_at	down	0.028154459	tubulin, alpha 1 (testis specific)
37840_at	up	0.02820166	cyclic nucleotide gated channel alpha 1
40146_at	down	0.028209265	RAP1B, member of RAS oncogene family
41002_at	up	0.028243866	solute carrier family 16 (monocarboxylic acid transporters), member 5
32012_at	up	0.028268131	pecanex homolog (Drosophila)
31984_at	up	0.028270556	
41294_at	up	0.02828124	keratin 7
41633_at	up	0.028282157	sentrin/SUMO-specific protease 3
32184_at	down	0.028317805	LIM domain only 2 (rhombotin-like 1)
40913_at	down	0.028333047	ATPase, Ca++ transporting, plasma membrane 4
33996_at	up	0.028357358	neuromedin B receptor
34640_at	up	0.028368648	transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1), albumin proximal factor
38962_at	up	0.028378275	KIAA0298 gene product
37157_at	up	0.028380947	calbindin 2, 29kDa (calretinin)
2028_s_at	up	0.028383411	E2F transcription factor 1
38198_at	up	0.028391962	similar to RIKEN cDNA 2610307I21
1659_s_at	down	0.028544189	Ras homolog enriched in brain 2
38729_at	up	0.028553044	FK506 binding protein 4, 59kDa
33950_g_at	up	0.028656928	corticotropin releasing hormone receptor 2
41555_at	up	0.028666961	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
32946_r_at	up	0.028673572	mannose-binding lectin (protein C) 2, soluble (opsonic defect)
36981_at	down	0.028721449	signal recognition particle 9kDa
31500_at	up	0.028739978	N-myc downstream regulated gene 1
105_at	up	0.028747273	nuclear receptor subfamily 1, group I, member 3
37369_s_at	up	0.028795072	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
1900_at	up	0.028796398	retinoblastoma 1 (including osteosarcoma)
37358_at	down	0.028871178	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
1062_g_at	down	0.028894304	interleukin 10 receptor, alpha
247_s_at	up	0.028908676	cytochrome P450, family 21, subfamily A, polypeptide 2
33184_at	up	0.028926665	guanylate cyclase activator 1A (retina)

40144_at	down	0.028926721	protein tyrosine phosphatase, non-receptor type substrate 1
1902_at	up	0.028929735	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
237_s_at	down	0.02901457	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
32871_at	up	0.029039566	
40129_at	down	0.029043392	protein kinase, DNA-activated, catalytic polypeptide
33852_at	down	0.029046277	TIA1 cytotoxic granule-associated RNA binding protein
41190_at	up	0.029048795	tumor necrosis factor receptor superfamily, member 25
34505_at	up	0.029085088	likely ortholog of mouse myocytic induction/differentiation originator
39911_at	up	0.029122116	hypothetical protein LOC51257
34334_at	up	0.029129367	ephrin-B2
32819_at	down	0.029198273	histone 1, H2bk
40012_at	up	0.02922851	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
1505_at	up	0.029239491	thymidylate synthetase
35814_at	down	0.029305093	dendritic cell protein
39955_at	up	0.029314355	deleted in lymphocytic leukemia, 2
37989_at	up	0.029335797	parathyroid hormone-like hormone
33416_at	up	0.029369792	KIAA1049 protein
41678_at	up	0.029375379	EphB2
41757_at	down	0.029390472	VAMP (vesicle-associated membrane protein)-associated protein B and C
35981_at	up	0.029401129	regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein)
32534_f_at	up	0.029407674	vesicle-associated membrane protein 5 (myobrevin)
716_at	up	0.029510223	gamma-glutamyltransferase-like activity 1
41336_at	up	0.029552307	DKFZP566O1646 protein
34774_at	down	0.029555309	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile)
1784_s_at	down	0.029583432	retinoblastoma binding protein 1
1517_at	up	0.029610936	cytochrome P450, family 2, subfamily F, polypeptide 1
40700_at	up	0.029668614	SP140 nuclear body protein
40323_at	up	0.029749549	CD38 antigen (p45)
37238_s_at	up	0.029796885	membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase

2086_s_at	up	0.029837041	TYRO3 protein tyrosine kinase
34351_at	up	0.029891028	phospholipase C, gamma 1 (formerly subtype 148)
467_at	down	0.029903899	osteoclast stimulating factor 1
35571_at	up	0.029924365	coagulation factor II (thrombin) receptor-like 3
33965_at	up	0.029960532	chemokine (C-C motif) ligand 1
41696_at	up	0.029980756	hypothetical protein MGC3077
36285_at	up	0.030018837	potassium inwardly-rectifying channel, subfamily J, member 4
322_at	up	0.030077773	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55 gamma)
38498_at	up	0.030096154	crystallin, beta B2
40836_s_at	up	0.030118354	heterogeneous nuclear ribonucleoprotein H3 (2H9)
232_at	up	0.030119073	laminin, gamma 1 (formerly LAMB2)
39174_at	down	0.030122401	nuclear receptor coactivator 4
37755_at	up	0.0301373	BTB (POZ) domain containing 3
39967_at	up	0.030138107	leucine zipper, down-regulated in cancer 1
38897_at	up	0.030160347	solute carrier family 7 (cationic amino acid transporter, y+ system member 4)
2050_s_at	down	0.030191058	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
35020_at	up	0.030204148	paired-like homeobox 2b
32505_at	up	0.030207295	NS1-associated protein 1
33302_at	up	0.030208659	sarcospan (Kras oncogene-associated gene)
33799_at	down	0.030209223	seven in absentia homolog 2 (Drosophila)
40840_at	up	0.03025459	peptidylprolyl isomerase F (cyclophilin F)
191_at	up	0.030325967	mucin 8, tracheobronchial
35090_g_at	up	0.030333092	neuregulin 2
40068_at	down	0.030347738	syntaxin 5A
39049_at	down	0.030357581	chromosome 6 open reading frame 9
34067_at	up	0.030369064	
35930_at	up	0.030372209	testis specific protein, Y-linked
33459_at	up	0.03040696	
37418_at	up	0.030409086	POU domain, class 2, transcription factor 2
34149_at	up	0.030409172	pleiotropic regulator 1 (PRL1 homolog, Arabidopsis)
41085_at	up	0.030435923	polymerase (DNA directed), epsilon 2 (p59 subunit)
40783_s_at	up	0.030449434	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide

892_at	up	0.030460619	transmembrane 4 superfamily member 1
40203_at	down	0.030488383	putative translation initiation factor
32002_at	up	0.030532859	GDNF family receptor alpha 3
37463_r_at	up	0.030546476	splicing factor 3a, subunit 2, 66kDa
38714_at	up	0.03055242	glycophorin A (includes MN blood group)
34726_at	up	0.030570264	calcium channel, voltage-dependent, beta 3 subunit
41374_at	up	0.030608379	ribosomal protein S6 kinase, 70kDa, polypeptide 2
36023_at	down	0.030629492	proline-rich protein HaeIII subfamily 1
36742_at	up	0.030653119	tripartite motif-containing 15
36771_at	up	0.030722552	cannabinoid receptor 2 (macrophage)
159_at	up	0.030730643	vascular endothelial growth factor C
AFFX-CreX-5_at	up	0.030730678	
39429_at	up	0.030749245	UV radiation resistance associated gene
34463_at	up	0.030750243	deoxyribonuclease I
824_at	down	0.030756422	glutathione-S-transferase like; glutathione transferase omega
35593_at	up	0.030776042	amine oxidase, copper containing 2 (retina-specific)
1090_f_at	up	0.030790531	vacuolar protein sorting 4B (yeast)
33576_at	up	0.03087025	KIAA0918 protein
923_at	up	0.030878031	ubiquitin-like 4
39607_at	up	0.030920096	myotubularin related protein 9
34554_at	up	0.030941865	glycine receptor, alpha 2
1858_at	up	0.030996193	tumor necrosis factor (ligand) superfamily, member 6
36433_at	up	0.031004583	glycine receptor, alpha 3
1427_g_at	down	0.031021674	Src-like-adaptor
634_at	up	0.031040949	protease, serine, 8 (prostasin)
32700_at	down	0.031048619	guanylate binding protein 2, interferon-inducible
38492_at	up	0.031061258	kynureninase (L-kynurenine hydrolase)
34127_at	up	0.031061577	organic cationic transporter-like 3
1153_f_at	up	0.031069865	chorionic gonadotropin, beta polypeptide
35102_at	up	0.031116602	zinc finger protein
35325_at	down	0.031161778	RAB14, member RAS oncogene family
35638_at	up	0.031168273	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related
37389_at	down	0.031316111	small acidic protein
31961_r_at	up	0.031323988	

36439_at	up	0.031332099	
32254_at	up	0.031358273	vesicle-associated membrane protein 2 (synaptobrevin 2)
36701_at	up	0.03135917	
1628_at	up	0.031360464	
37397_at	down	0.031394119	platelet/endothelial cell adhesion molecule (CD31 antigen)
39420_at	down	0.031398275	DNA-damage-inducible transcript 3
32228_at	up	0.031413344	adaptor-related protein complex 2, alpha 2 subunit
32053_at	down	0.031474283	cyclin T2
36509_at	down	0.031476516	ribosomal protein L35a
36793_at	up	0.03149691	hypothetical protein AY099107
31941_s_at	up	0.031534979	ret finger protein-like 3
33999_f_at	up	0.031557766	
34924_at	up	0.031605825	kinesin family member 1B
37850_at	up	0.031616361	hypothetical protein dJ462O23.2
1853_at	up	0.031673028	wingless-type MMTV integration site family, member 1
32761_at	up	0.031711267	serine/arginine repetitive matrix 2
35848_at	down	0.031713305	retinoic acid induced 17
33058_at	up	0.03184771	cytokeratin type II
635_s_at	up	0.031851567	protein phosphatase 2, regulatory subunit B (B56), beta isoform
35411_at	up	0.031857375	chromosome 16 open reading frame 7
32520_at	up	0.031885468	nuclear receptor subfamily 1, group D, member 1
31915_at	up	0.031889645	dystrophin related protein 2
36714_at	up	0.031890786	nuclear receptor subfamily 2, group C, member 2
34847_s_at	up	0.031912545	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta
424_s_at	up	0.031967116	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)
31414_at	up	0.031975481	testis-specific transcript, Y-linked 2
32896_at	up	0.032009199	
35417_at	up	0.03208939	cubilin (intrinsic factor-cobalamin receptor)
35263_at	down	0.032117131	eukaryotic translation initiation factor 4E binding protein 2
1573_at	up	0.032134508	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)
792_s_at	up	0.032185586	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)
33232_at	down	0.032194657	cysteine-rich protein 1 (intestinal)
37545_at	up	0.032225183	secretory carrier membrane protein 5

41630_at	up	0.032231183	CGI-62 protein
35285_at	up	0.032272611	solute carrier family 4, sodium bicarbonate cotransporter, member 4
41618_at	up	0.032282842	collagen, type XVII, alpha 1
39497_at	up	0.032294796	hypothetical protein FLJ10803
41324_g_at	up	0.032328237	forkhead box M1
36716_at	up	0.032332777	adrenergic, alpha-1A-, receptor
38191_at	up	0.032337124	KIAA0645 gene product
36315_l_at	up	0.032376572	Sec15B protein
34128_at	up	0.032402682	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
33356_at	up	0.032468294	trinucleotide repeat containing 3
31566_at	up	0.032480202	
37811_at	up	0.032501096	calcium channel, voltage-dependent, alpha 2/delta subunit 2
37035_at	down	0.03252466	stress-associated endoplasmic reticulum protein 1
37165_f_at	up	0.032565127	Rhesus blood group, CcEe antigens
32499_at	up	0.032569682	Rho GDP dissociation inhibitor (GDI) gamma
36200_at	up	0.032605501	HLA-B associated transcript 8
31443_at	up	0.032611589	
38664_at	down	0.032630779	craniofacial development protein 1
423_at	down	0.0326721	Ewing sarcoma breakpoint region 1
39206_s_at	up	0.032698078	aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122)
41467_at	up	0.032750937	mutS homolog 5 (E. coli)
38755_at	up	0.032752728	Fas (TNFRSF6)-associated via death domain
34575_f_at	up	0.032809836	melanoma antigen, family A, 5
35553_at	up	0.032825078	TSPY-like
38221_at	up	0.032832296	connector enhancer of KSR-like (Drosophila kinase suppressor of ras)
35362_at	up	0.03290105	myosin X
35400_at	up	0.032907138	
221_s_at	up	0.032936681	phosphatidylinositol glycan, class A (paroxysmal nocturnal hemoglobinuria)
36093_at	up	0.032947133	KIAA0614 protein
36462_at	up	0.032953356	SMYD family member 5
1892_s_at	up	0.032967779	
38766_at	up	0.033003801	Snf2-related CBP activator protein
39276_g_at	up	0.033018192	calcium channel, voltage-dependent, L type, alpha 1D subunit
37922_at	up	0.033026389	transcobalamin II; macrocytic anemia

38390_at	up	0.033060083	component of oligomeric golgi complex 2
40916_at	down	0.033066997	hypothetical protein FLJ10097
36094_at	up	0.033067781	troponin T3, skeletal, fast
35184_at	down	0.033082679	KIAA0546 protein
35537_at	up	0.033137937	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain
40759_at	up	0.03313989	matrix metalloproteinase 16 (membrane-inserted)
38084_at	down	0.033140959	chromobox homolog 3 (HP1 gamma homolog, Drosophila)
38934_at	up	0.033155647	
35995_at	up	0.033159596	ZW10 Interactor
39000_at	up	0.033222247	N-myristoyltransferase 1
31791_at	up	0.033224619	tumor protein p73-like
31392_r_at	up	0.033262168	chromosome 1 open reading frame 1
36248_at	up	0.033265588	NAG-5 protein
35564_at	up	0.033280281	
223_at	down	0.033309012	ubiquitin-conjugating enzyme E2L 3
37781_at	up	0.033368336	neurexin 2
40295_at	up	0.033391699	copine VI (neuronal)
35191_at	up	0.033424161	KIAA0375 gene product
171_at	down	0.033442103	von Hippel-Lindau binding protein 1
39046_at	down	0.033467681	histone H2A.F/Z variant
36369_at	up	0.033478368	polymerase I and transcript release factor
1789_at	down	0.033529093	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)
33121_g_at	down	0.033549364	regulator of G-protein signalling 10
32659_at	down	0.033576868	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa
37234_at	up	0.033609251	kininogen
457_s_at	down	0.033618854	ubiquitin-like 1 (sentrin)
34173_s_at	up	0.033652359	contactin 5
34604_at	up	0.0336552	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4
1155_at	up	0.033705413	v-myc myelocytomatosis viral oncogene homolog 2 (avian)
35316_at	down	0.033716548	Ras-related GTP-binding protein
34355_at	down	0.033779716	methyl CpG binding protein 2 (Rett syndrome)
1156_at	up	0.033793231	Sp1 transcription factor
36516_at	up	0.033803067	zinc finger protein ZFP100
31321_at	up	0.033837372	pancreatic beta cell growth factor
40097_at	down	0.033852776	eukaryotic translation initiation factor 1A, Y chromosome



33839_at	up	0.033863607	inositol 1,4,5-triphosphate receptor, type 2
34626_at	up	0.033878835	hypermethylated in cancer 1
326_i_at	down	0.03389412	
40239_g_at	up	0.033906971	G protein-coupled receptor, family C, group 5, member B
34722_at	up	0.033910912	tissue inhibitor of metalloproteinase 2
35454_at	up	0.033944357	KIAA0450 gene product
1613_s_at	up	0.033952839	ubiquitin specific protease 6 (Tre-2 oncogene)
35693_at	up	0.033996591	hippocalcin-like 1
1095_s_at	up	0.034001673	hepatocyte growth factor (hepapoietin A; scatter factor)
41573_at	down	0.034024859	Sp3 transcription factor
33677_at	down	0.034077303	ribosomal protein L24
41388_at	up	0.03408507	Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse)
32409_at	up	0.034121256	phosphatidylinositol glycan class O
37788_at	up	0.03412756	
38980_at	down	0.034131969	mitogen-activated protein kinase kinase kinase 7 interacting protein 2
34897_at	up	0.034163537	protein phosphatase 4, regulatory subunit 2
32221_at	down	0.034177991	mitochondrial ribosomal protein S18B
38323_at	down	0.034293103	carboxypeptidase, vitellogenic-like
33570_at	up	0.034304188	NK2 transcription factor related, locus 5 (Drosophila)
36318_at	up	0.034313433	homolog of rat orphan transporter v7-3
35967_at	up	0.034376104	aryl hydrocarbon receptor nuclear translocator
31659_at	up	0.034390954	DKFZP434K091 protein
31661_at	up	0.034425691	
41756_at	down	0.034438173	XPA binding protein 1
33046_f_at	up	0.034440875	empty spiracles homolog 1 (Drosophila)
37666_at	up	0.034522353	proteasome (prosome, macropain) subunit, beta type, 5
32425_at	up	0.034526343	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)
40571_at	down	0.03453232	myosin VA (heavy polypeptide 12, myoxin)
33219_at	down	0.034561079	pVHL-interacting deubiquitinating enzyme 1
32267_at	up	0.034563899	zinc finger protein 345
31510_s_at	down	0.034573927	H3 histone, family 3B (H3.3B)
39652_at	up	0.034588394	chemokine (C motif) ligand 1
1782_s_at	up	0.034594134	stathmin 1/oncoprotein 18
38819_at	up	0.034640515	PTK7 protein tyrosine kinase 7

39221_at	down	0.034659495	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2
37813_at	up	0.034669603	
38056_at	up	0.034690705	KIAA0195 gene product
527_at	up	0.034691647	centromere protein A, 17kDa
33137_at	up	0.034815653	latent transforming growth factor beta binding protein 4
34743_at	up	0.03491869	scribble
40954_at	up	0.034930625	FXD domain containing ion transport regulator 2
32739_at	up	0.034938417	phosphoglucomutase 3
39747_at	down	0.034979203	polymerase (RNA) II (DNA directed) polypeptide G
40672_at	up	0.035009921	kynureninase (L-kynurenine hydrolase)
34607_at	up	0.0350146	inducible T-cell co-stimulator
32991_f_at	up	0.035068269	amelogenin (Y chromosome)
31314_at	up	0.035072962	bone morphogenetic protein 3 (osteogenic)
33178_at	up	0.035088856	jagged 1 (Alagille syndrome)
37832_at	up	0.035109738	DKFZP564I122 protein
802_at	down	0.035128062	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa
32025_at	down	0.035193294	transcription factor 7-like 2 (T-cell specific, HMG-box)
39086_g_at	down	0.035197215	single-stranded DNA binding protein
39777_at	down	0.035201873	protein associated with Myc
35260_at	up	0.03524273	Mlx interactor
33247_at	down	0.03528389	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
39179_at	up	0.035361402	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)
35038_at	up	0.035365152	myosin binding protein C, cardiac
35742_at	up	0.0353725	hypothetical gene BC008967
38308_g_at	up	0.035420841	neurochondrin
37177_at	down	0.035452242	CD58 antigen, (lymphocyte function-associated antigen 3)
38066_at	up	0.035462531	NAD(P)H dehydrogenase, quinone 1
38528_at	up	0.035497003	acetyl-Coenzyme A carboxylase alpha
32248_at	down	0.035497896	hypothetical protein PRO2730
32548_at	down	0.035500275	inactive progesterone receptor, 23 kD
32263_at	up	0.035509211	cyclin B2
32622_at	up	0.03554138	dynamitin 2

35327_at	down	0.03561689	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa
37001_at	down	0.035620522	calpain 2, (mII) large subunit
35207_at	up	0.035647227	sodium channel, nonvoltage-gated 1 alpha
37697_s_at	down	0.035661664	voltage-dependent anion channel 2
34637_f_at	up	0.035677011	alcohol dehydrogenase 1A (class I), alpha polypeptide
40238_at	up	0.035681038	G protein-coupled receptor, family C, group 5, member B
41657_at	up	0.035748093	serine/threonine kinase 11 (Peutz-Jeghers syndrome)
38072_at	down	0.035800174	hypothetical protein dJ465N24.2.1
35949_at	up	0.035817369	KIAA0774 protein
39133_at	down	0.035822484	GCN5 general control of amino-acid synthesis 5-like 1 (yeast)
440_at	up	0.035839885	nuclear factor I/C (CCAAT-binding transcription factor)
39032_at	down	0.035842888	transforming growth factor beta-stimulated protein TSC-22
36859_at	up	0.03584934	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
32075_at	up	0.035852074	zinc finger protein 161 homolog (mouse)
41007_at	up	0.03590906	myozenin 3
37908_at	down	0.035935871	guanine nucleotide binding protein (G protein), gamma 11
39111_s_at	down	0.035951483	peptidylprolyl isomerase (cyclophilin)-like 2
39390_at	down	0.035991974	nucleoporin 133kDa
1536_at	up	0.036029396	CDC6 cell division cycle 6 homolog (S. cerevisiae)
40810_at	down	0.036034327	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
39015_f_at	up	0.036068618	keratin 6A
31439_f_at	up	0.036084452	Rhesus blood group, CcEe antigens
38291_at	up	0.036104104	proenkephalin
39217_at	up	0.036118403	
728_at	up	0.03612594	
40267_s_at	up	0.036136261	KIAA1036 protein
35442_at	up	0.036186437	KIAA0792 gene product
39034_at	down	0.036243812	DKFZP564O123 protein
33227_at	down	0.036245055	interleukin 10 receptor, beta
39927_at	up	0.036258257	Rho GTPase activating protein 5
31365_f_at	up	0.036274538	nuclear factor of activated T-cells 5, tonicity-responsive

883_s_at	up	0.036301176	pim-1 oncogene
1512_at	down	0.036307971	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
35011_at	down	0.036313265	HECT type E3 ubiquitin ligase
38204_at	up	0.036318873	KIAA0406 gene product
37381_g_at	down	0.036360287	general transcription factor IIB
162_at	up	0.036372555	ubiquitin specific protease 11
34568_at	up	0.036382821	keratin, hair, acidic, 3B
34160_at	down	0.036395515	actin, gamma 1
41872_at	up	0.036421973	deafness, autosomal dominant 5
40636_at	up	0.036435919	flotillin 1
1382_at	down	0.036530269	replication protein A1, 70kDa
36360_at	up	0.036567094	KIAA0507 protein
39542_at	up	0.036640558	ectodermal-neural cortex (with BTB-like domain)
1765_at	up	0.036649057	caspase 10, apoptosis-related cysteine protease
837_s_at	down	0.03665956	malic enzyme 1, NADP(+)-dependent, cytosolic
1949_at	up	0.036688112	angiopoietin 1
37135_f_at	up	0.036721619	glutamate receptor, ionotropic, N-methyl D-aspartate 1
40754_at	up	0.036753843	general transcription factor IIH, polypeptide 3, 34kDa
39288_at	up	0.036831137	nectin-like protein 1
33580_r_at	up	0.036856676	galanin receptor 3
990_at	up	0.036936172	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
41780_at	down	0.036941323	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
31412_at	up	0.036983521	PTPN13-like, Y-linked
38544_at	up	0.036991342	inhibin, alpha
39760_at	down	0.036998817	quaking homolog, KH domain RNA binding (mouse)
160026_at	up	0.037003493	protein kinase, X-linked
37844_at	down	0.037057085	class I cytokine receptor
38627_at	up	0.037109589	hepatic leukemia factor
AFFX-M27830_3_at	up	0.037136535	
39601_at	up	0.037182176	Ras association (RalGDS/AF-6) domain family 1
39212_at	up	0.037250199	hypothetical protein FLJ11191
35451_s_at	up	0.037307942	SCAN domain containing 2

34064_s_at	up	0.037309471	natural cytotoxicity triggering receptor 2
36956_at	up	0.037350527	solute carrier family 20 (phosphate transporter), member 2
41355_at	down	0.037373862	B-cell CLL/lymphoma 11A (zinc finger protein)
39208_i_at	down	0.037381904	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)
38415_at	down	0.037413264	protein tyrosine phosphatase type IVA, member 2
38445_at	up	0.037433428	actin related protein 2/3 complex, subunit 2, 34kDa
1322_at	up	0.037477325	cathepsin K (pseudodysostosis) fatty acid binding protein 6, ileal (gastrotrypin)
38466_at	up	0.037501653	
36779_at	up	0.037509117	
1295_at	down	0.037566519	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)
37423_at	up	0.037568568	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
41406_at	down	0.037620194	hypothetical protein FLJ21919
34112_r_at	up	0.037686408	
34038_at	up	0.037720153	solute carrier family 6 (neurotransmitter transporter, GABA), member 13
38781_at	up	0.037740959	glutathione S-transferase A2 empty spiracles homolog 1 (Drosophila)
33045_r_at	up	0.037754364	
33420_g_at	down	0.037813208	apoptosis inhibitor 5
34877_at	down	0.037874468	Janus kinase 1 (a protein tyrosine kinase)
39920_r_at	up	0.037908818	C1q-related factor
40617_at	down	0.037913324	hypothetical protein FLJ20274 T-box 6
31602_at	up	0.037939657	
39190_s_at	up	0.03794319	
38158_at	up	0.037955678	extra spindle poles like 1 (S. cerevisiae)
39563_at	up	0.037962522	KIAA0268 protein
38393_at	down	0.037967247	KIAA0247 gene product
37986_at	down	0.038002259	erythropoietin receptor
33293_at	up	0.038041132	Fas apoptotic inhibitory molecule 2
35146_at	up	0.0380469	transforming growth factor beta 1 induced transcript 1
34566_at	up	0.038085141	calcitonin-related polypeptide, beta

41246_at	up	0.038116844	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2
39426_at	down	0.03813583	transcription elongation regulator 1 (CA150)
39608_at	up	0.038173191	single-minded homolog 2 (Drosophila)
41858_at	up	0.038174864	FGF receptor activating protein 1
37668_at	down	0.038273197	complement component 1, q subcomponent binding protein
35947_at	up	0.038343221	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)
41129_at	down	0.038356011	KIAA0033 protein
40268_at	up	0.038387842	FOS-like antigen 2
36617_at	up	0.038390439	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
39946_at	up	0.038392089	pancreatitis-associated protein
35297_at	down	0.038407506	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
41172_at	down	0.038407527	retinol dehydrogenase 11 (all-trans and 9-cis)
32980_f_at	down	0.038440496	histone 1, H2bc
39364_s_at	up	0.038449579	protein phosphatase 1, regulatory (inhibitor) subunit 3C
33060_g_at	up	0.038481349	
39109_at	up	0.038509158	chromosome 20 open reading frame 1
2041_l_at	up	0.038513823	v-abl Abelson murine leukemia viral oncogene homolog 1
37984_s_at	down	0.038552881	ADP-ribosylation factor 6
36746_s_at	up	0.038564507	calcitonin receptor
39616_at	up	0.038593624	
1270_at	up	0.038616745	RAP1, GTPase activating protein 1
35464_at	up	0.038622074	interleukin 11
41187_at	down	0.038647669	myosin regulatory light chain MRLC2
39143_at	down	0.038679527	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
34260_at	up	0.038707405	KIAA0683 gene product
37567_at	up	0.038711751	sal-like 2 (Drosophila)
35612_at	up	0.038714873	DKFZP564P1916 protein
37858_at	up	0.038730644	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase
34984_at	up	0.038737233	transient receptor potential cation channel, subfamily C, member

33949_at	up	0.03874733	corticotropin releasing hormone receptor 2
342_at	up	0.038767213	ectonucleotide pyrophosphatase/phosphodiesterase 1
33052_at	up	0.038797008	phospholipase A2, group X
41423_at	up	0.038802753	calsyntenin 3
37112_at	down	0.038914634	chromosome 6 open reading frame 32
1754_at	up	0.038967239	death-associated protein 6
33025_at	up	0.038968578	chromosome 20 open reading frame 10
627_g_at	up	0.039082	arginine vasopressin receptor 1B
34731_at	down	0.039093403	programmed cell death 11
32568_at	up	0.039115444	BTG family, member 3
36881_at	down	0.039125362	electron-transfer-flavoprotein, beta polypeptide
41686_s_at	up	0.039157522	NY-REN-7 antigen
38487_at	up	0.039168582	stabilin 1
40417_at	down	0.039177693	chaperonin containing TCP1, subunit 5 (epsilon)
35849_at	up	0.039215248	phosphatidylserine receptor
33243_at	down	0.039241844	TNF-induced protein
32346_at	up	0.039243412	
40461_at	up	0.039253806	triple homeobox 1
40028_at	up	0.039264393	LOC92346
34932_at	up	0.039274406	melanoma antigen, family C, 1
37648_at	up	0.039293338	KIAA0153 protein
32542_at	down	0.039325252	four and a half LIM domains 1
39209_r_at	down	0.039349881	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)
41819_at	down	0.039389573	FYN binding protein (FYB-120/130)
31492_at	down	0.039426982	muscle specific gene
38481_at	down	0.039431725	replication protein A1, 70kDa
36004_at	up	0.039498058	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma
31551_at	up	0.039538216	gamma-aminobutyric acid (GABA) receptor, rho 2
40613_at	down	0.039628778	chromosome 6 open reading frame 62
37970_at	up	0.039662257	mitogen-activated protein kinase 8 interacting protein 3
1666_at	up	0.039665359	interferon, alpha 1
115_at	down	0.039688446	thrombospondin 1
2037_s_at	up	0.039733454	ribosomal protein S6 kinase, 70kDa, polypeptide 1
38152_at	up	0.039735408	loss of heterozygosity, 11, chromosomal region 2, gene A
36169_at	down	0.039738748	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa

AFFX-BioB-3_at	up	0.039745177	
40353_at	up	0.039779913	
31409_at	up	0.039789728	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10
37049_g_at	up	0.039808882	translocase of outer mitochondrial membrane 34
36473_at	up	0.039827121	ubiquitin specific protease 20
35743_at	up	0.039844257	cleavage and polyadenylation specific factor 4, 30kDa
38444_at	up	0.039897913	cysteine and glycine-rich protein 3 (cardiac LIM protein)
32557_at	up	0.039917401	U2 small nuclear ribonucleoprotein auxiliary factor (65kD)
34539_at	up	0.039968141	olfactory receptor, family 7, subfamily A, member 126 pseudogene
36851_g_at	up	0.040105766	Putative prostate cancer tumor suppressor
32648_at	up	0.040119322	delta-like 1 homolog (Drosophila)
39030_at	up	0.040121358	Rab acceptor 1 (prenylated)
39391_at	down	0.04013934	associated molecule with the SH3 domain of STAM
41822_at	up	0.040160905	zinc finger protein
32818_at	up	0.040201801	tenascin C (hexabrachion)
39313_at	up	0.040229309	protein kinase, lysine deficient 1
37926_at	up	0.040231459	Kruppel-like factor 5 (intestinal)
875_g_at	up	0.040259866	chemokine (C-C motif) ligand 2
31487_at	up	0.040270313	fasciculation and elongation protein zeta 2 (zygin II)
38613_at	up	0.040286427	putative cyclin G1 interacting protein
2007_g_at	up	0.040353971	Janus kinase 3 (a protein tyrosine kinase, leukocyte)
39136_at	down	0.040366437	oxidative-stress responsive 1
41782_g_at	up	0.0403846	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
35749_at	up	0.040386806	transcriptional adaptor 3 (NGG1 homolog, yeast)-like
39331_at	up	0.040419286	tubulin, beta polypeptide
36476_at	down	0.040425881	bromodomain containing 8
40247_at	up	0.040437893	solute carrier family 9 (sodium/hydrogen exchanger), isoform 7
40167_s_at	down	0.040463083	likely ortholog of mouse WD-40-repeat-containing protein with a SOCS box 2
32034_at	down	0.040506981	zinc finger protein 217
40567_at	down	0.040518867	tubulin, alpha 3
40691_at	down	0.040548176	zinc finger protein 274
37005_at	up	0.040561003	neuroblastoma, suppression of tumorigenicity 1



40371_at	up	0.040591204	dopamine receptor D2
31388_at	up	0.040627727	early lymphoid activation protein
AFFX-CreX-3_at	up	0.040647806	
41499_at	up	0.040698611	v-ski sarcoma viral oncogene homolog (avian)
38131_at	up	0.040768509	prostaglandin E synthase
40266_at	up	0.04078716	KIAA1036 protein
39324_at	up	0.040788061	
1154_at	up	0.040819001	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
413_at	up	0.040842837	homeo box D9
34299_at	down	0.040881701	zinc finger protein 278
39050_at	up	0.040889932	poly(A) binding protein, nuclear 1
35408_i_at	down	0.040944508	zinc finger protein 44 (KOX 7)
41720_r_at	up	0.040965049	fatty acid desaturase 1
1392_at	up	0.041028012	G protein-coupled receptor kinase 6
37011_at	down	0.041037942	allograft inflammatory factor 1
40430_at	up	0.041117487	hypothetical protein FLJ35779
40439_at	down	0.041157278	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)
36745_at	up	0.041195119	
39105_at	down	0.041201015	vasodilator-stimulated phosphoprotein
37941_at	up	0.041220219	myosin binding protein C, fast type
1806_at	up	0.041223406	MCF.2 cell line derived transforming sequence
34049_at	down	0.041282808	
41718_g_at	up	0.041288593	fatty acid desaturase 1
34738_at	up	0.041289183	serine hydroxymethyltransferase 1 (soluble)
40379_at	up	0.041411241	cytochrome P450, family 2, subfamily E, polypeptide 1
32646_at	up	0.041464958	KIAA0449 protein
720_at	up	0.041465792	heat shock transcription factor 4
33151_s_at	up	0.041485117	disrupter of silencing 10
39970_at	up	0.041555279	nuclear receptor subfamily 0, group B, member 1
375_at	up	0.041589703	glutathione S-transferase theta 1
33697_at	up	0.041601882	purinergic receptor P2X, ligand-gated ion channel, 7
420_at	up	0.041622259	melanocortin 2 receptor (adrenocorticotrophic hormone)
40733_f_at	up	0.041645239	msh homeo box homolog 2 (Drosophila)
763_at	down	0.041702481	glia maturation factor, beta
2005_s_at	up	0.0417241	Janus kinase 3 (a protein tyrosine kinase, leukocyte)

41651_at	down	0.041743121	KIAA1033 protein
35991_at	down	0.041767326	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)
38814_at	down	0.041813234	ATPase, H <sup>+</sup> transporting, lysosomal 13kDa, V1 subunit G isoform 1
38548_at	up	0.041829912	cytochrome P450, family 2, subfamily C, polypeptide 8
38312_at	up	0.041984212	
37955_at	down	0.042020127	transmembrane protein 4
31357_at	up	0.042037339	
34192_at	down	0.042048499	KIAA0532 protein
33336_at	up	0.042053513	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)
632_at	up	0.042123503	glycogen synthase kinase 3 alpha
1168_at	up	0.042146694	protocadherin beta 17 pseudogene
38794_at	down	0.042176671	upstream binding transcription factor, RNA polymerase I
36562_at	up	0.042240759	KIAA0427 gene product
36952_at	up	0.042241044	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
37994_at	down	0.042302692	fragile X mental retardation 1
1750_at	up	0.042309315	phenylalanine-tRNA synthetase-like
1914_at	up	0.042374368	cyclin A1
37330_at	up	0.0424156	aldehyde dehydrogenase 4 family, member A1
36939_at	up	0.042424587	glycoprotein M6A
32573_at	down	0.042442348	splicing factor, arginine/serine-rich 9
33997_at	up	0.042551104	
1875_f_at	up	0.042561561	postmeiotic segregation increased 2-like 3
35953_at	up	0.042571185	carboxypeptidase N, polypeptide 1, 50kD
32258_r_at	down	0.042616045	telomeric repeat binding factor (NIMA-interacting) 1
32493_at	up	0.04264112	thyrotrophic embryonic factor
41557_at	down	0.042735256	KIAA0052 protein
35673_at	up	0.042751453	Rho guanine nucleotide exchange factor (GEF) 5
1255_g_at	up	0.042771637	guanylate cyclase activator 1A (retina)
648_at	up	0.042778333	arginine vasopressin receptor 1B
1574_s_at	up	0.042812441	interleukin 4
1380_at	up	0.042829999	fibroblast growth factor 7 (keratinocyte growth factor)
40701_at	up	0.042832741	ubiquitin specific protease 13 (isopeptidase T-3)

33945_at	down	0.042849117	tumor necrosis factor (ligand) superfamily, member 5 (hyper-IgM syndrome)
40731_at	up	0.04287054	chromobox homolog 5 (HP1 alpha homolog, Drosophila)
33637_g_at	up	0.042880647	cancer/testis antigen 1
1115_at	down	0.042942517	platelet factor 4 (chemokine (C-X-C motif) ligand 4)
37977_at	up	0.042975756	deltex homolog 2 (Drosophila)
34809_at	down	0.042989623	KIAA0999 protein
38105_at	down	0.04300635	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4
33522_at	up	0.043053962	agouti signaling protein, nonagouti homolog (mouse)
32717_at	up	0.043086938	neuralized-like (Drosophila)
1377_at	down	0.043126879	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
36596_r_at	up	0.043217487	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
AFFX-BioDn-3_at	up	0.043247969	
1477_s_at	up	0.04330999	cytochrome P450, family 2, subfamily C, polypeptide 18
39842_at	up	0.043318734	cytokine receptor-like factor 1
1903_at	down	0.043361718	
40777_at	down	0.04336893	catenin (cadherin-associated protein), beta 1, 88kDa
34636_at	up	0.043370973	arachidonate 15-lipoxygenase
39645_r_at	up	0.043372248	arrestin 3, retinal (X-arrestin)
41764_at	down	0.043388296	apolipoprotein C-I
36488_at	down	0.043398698	EGF-like-domain, multiple 5
491_at	up	0.04341321	protein tyrosine phosphatase, receptor type, G
37218_at	up	0.043488344	BTG family, member 3
33498_at	up	0.043497555	regenerating islet-derived-like, pancreatic stone protein-like, pancreatic thread protein-like (rat)
640_at	up	0.043523098	angiotensin II receptor-like 2
36845_at	down	0.043540169	nuclear matrix protein NXP2
35783_at	down	0.043700506	vesicle-associated membrane protein 3 (cellubrevin)
38529_at	up	0.043708018	acetyl-Coenzyme A carboxylase beta
31947_r_at	up	0.043725153	forkhead box G1A
40689_at	down	0.043739673	sel-1 suppressor of lin-12-like (C. elegans)

34088_at	up	0.043767248	neurexophilin 4
34884_at	up	0.043790003	carbamoyl-phosphate synthetase 1, mitochondrial
35056_at	up	0.043793206	arylsulfatase F
37348_s_at	down	0.043822957	high mobility group nucleosomal binding domain 3
40132_g_at	down	0.04383039	folistatin-like 1
34422_r_at	up	0.043832201	uncoupling protein 3 (mitochondrial, proton carrier)
36659_at	up	0.043859511	collagen, type IV, alpha 2
35722_at	down	0.04386591	UPF2 regulator of nonsense transcripts homolog (yeast)
34356_at	down	0.043974258	SRB7 suppressor of RNA polymerase B homolog (yeast)
33540_at	up	0.044014718	
296_at	down	0.04402855	
41147_at	down	0.044084481	hypothetical protein MGC4276 similar to CG8198
40610_at	down	0.044101702	zinc finger RNA binding protein
41208_at	down	0.044106895	S164 protein
31986_at	up	0.044122485	
39462_s_at	up	0.044182359	cyclin M2
40958_at	up	0.044246117	KIAA0599 protein
39063_at	up	0.044305104	actin, alpha, cardiac muscle
36754_at	up	0.044401821	adenylate cyclase activating polypeptide 1 (pituitary)
975_at	up	0.04454837	serine/threonine kinase 18
41543_at	up	0.044555245	lymphoid nuclear protein related to AF4
39821_s_at	up	0.04462269	growth arrest and DNA-damage-inducible, beta
38942_r_at	up	0.044661343	AD024 protein
39834_at	up	0.044677883	cholinergic receptor, nicotinic, epsilon polypeptide
41158_at	up	0.044679844	proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated)
35954_at	up	0.044713	prodynorphin
38952_s_at	up	0.04475812	collagen, type XIII, alpha 1
1731_at	up	0.044857816	platelet-derived growth factor receptor, alpha polypeptide
40067_at	down	0.044859698	E74-like factor 1 (ets domain transcription factor)
38174_at	up	0.044860824	pleckstrin and Sec7 domain protein
1473_s_at	up	0.044866751	v-myb myeloblastosis viral oncogene homolog (avian)
34475_at	up	0.044903408	

39095_at	up	0.044919175	myosin, heavy polypeptide 7, cardiac muscle, beta
34771_at	up	0.044938431	phosphatidic acid phosphatase type 2C
39824_at	up	0.04494232	protein tyrosine phosphatase type IVA, member 3
33583_r_at	up	0.044980903	RNA binding motif, single stranded interacting protein
38567_at	down	0.045086218	CD1D antigen, d polypeptide
33213_g_at	up	0.04509451	ribosome binding protein 1 homolog 180kDa (dog)
34799_at	up	0.045130417	intraflagellar transport protein IFT20
31708_at	down	0.045135218	ribosomal protein L30
39187_at	up	0.045161232	runt-related transcription factor 2
39175_at	down	0.045229902	phosphofructokinase
38340_at	up	0.045251115	huntingtin interacting protein-1-related
38919_at	up	0.045257342	chromosome 6 open reading frame 84
32836_at	up	0.045281983	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)
AFFX-BioB-M_st	up	0.045314371	
110_at	up	0.045320404	chondroitin sulfate proteoglycan 4 (melanoma-associated)
36457_at	down	0.045332883	guanine monophosphate synthetase
1038_s_at	down	0.045424969	interferon gamma receptor 1
32707_at	up	0.045428446	katanin p60 (ATPase-containing) subunit A 1
40772_at	up	0.04548016	hypothetical protein FLJ22269
36995_at	up	0.045488385	alpha-1-microglobulin/bikunin precursor
37439_at	up	0.045504275	solute carrier family 30 (zinc transporter), member 4
32023_at	up	0.045513124	
40975_s_at	up	0.04553262	tuftelin interacting protein 11
39684_at	up	0.045568029	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)
33534_at	up	0.045610323	endothelial cell-specific molecule 1
39738_at	down	0.045611646	myosin, heavy polypeptide 9, non-muscle
36171_at	down	0.045654778	activated RNA polymerase II transcription cofactor 4
34885_at	up	0.045703542	synaptogyrin 2
32525_r_at	up	0.045882979	junctional adhesion molecule 3
41206_r_at	down	0.045915305	cytochrome c oxidase subunit VIa polypeptide 1

31858_at	down	0.045925116	nuclear transport factor 2
32480_at	up	0.045946721	homeo box C4
37801_at	up	0.045990579	ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit a isoform 2
41211_at	up	0.045997988	RNA binding motif protein 12
40326_at	up	0.046028247	cerebellin 1 precursor
35425_at	up	0.046028539	BarH-like homeobox 2
38447_at	up	0.046105867	adrenergic, beta, receptor kinase 1
36687_at	down	0.046108202	cytochrome c oxidase subunit VIIb
1648_at	up	0.046115812	oncostatin M receptor
41386_i_at	up	0.046126282	KIAA0346 protein
34182_at	up	0.046136684	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1
37084_at	up	0.04615034	lysozyme homolog
37102_at	up	0.046158495	breast cancer metastasis-suppressor 1
38888_at	up	0.046186078	leucine-rich, glioma inactivated 1
36333_at	down	0.046189903	ribosomal protein L7
33404_at	up	0.046205759	adenylyl cyclase-associated protein 2
41321_s_at	up	0.046241974	nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs)
1406_at	up	0.046355671	nuclear receptor subfamily 2, group C, member 1
33897_at	up	0.046389018	phosphatidylinositol 4-kinase type II
34280_at	up	0.046453241	gamma-aminobutyric acid (GABA) A receptor, epsilon
1037_at	up	0.046542336	B melanoma antigen
40901_at	down	0.046554909	striatin, calmodulin binding protein 3
38311_at	down	0.046571724	TGFB-induced factor 2 (TALE family homeobox)
37449_i_at	down	0.046577216	GNAS complex locus
506_s_at	up	0.046586309	signal transducer and activator of transcription 5A
38820_at	down	0.046590628	15 kDa selenoprotein
40138_at	up	0.046591745	COP9 subunit 6 (MOV34 homolog, 34 kD)
38075_at	down	0.046592172	synaptophysin-like protein
32705_at	up	0.04659497	cytochrome P450, family 3, subfamily A, polypeptide 7
38328_at	down	0.046624433	solute carrier family 25, member 13 (citrin)
33931_at	down	0.046631191	glutathione peroxidase 4 (phospholipid hydroperoxidase)
1388_g_at	down	0.046638995	vitamin D (1,25- dihydroxyvitamin D3) receptor
36396_at	up	0.046663781	
31878_at	down	0.046669447	ATP-binding cassette, sub-family F (GCN20), member 2
35727_at	down	0.046749257	uridine kinase-like 1

31824_at	up	0.046757144	malic enzyme 1, NADP(+)-dependent, cytosolic
34741_at	up	0.046861972	transcription factor Dp-2 (E2F dimerization partner 2)
39189_at	up	0.046938514	potassium voltage-gated channel, Shaw-related subfamily, member 4
37195_at	up	0.046947354	cytochrome P450, family 11, subfamily A, polypeptide 1
41778_at	up	0.046964409	solute carrier family 1 (neutral amino acid transporter), member 5
40561_at	up	0.046977023	T-cell leukemia, homeobox 2
31318_at	up	0.047010382	
31985_at	up	0.047097209	pleckstrin homology domain interacting protein
31571_at	up	0.047105137	polymerase (RNA) III (DNA directed) (32kD)
34179_at	up	0.047151817	zinc finger protein 297
39005_s_at	down	0.047173316	zinc finger protein 294
39634_at	up	0.047190272	slit homolog 2 (Drosophila)
38359_at	up	0.047233322	RAS guanyl releasing protein 2 (calcium and DAG-regulated)
39767_at	down	0.047273537	chaperonin containing TCP1, subunit 8 (theta)
35368_at	down	0.047276393	zinc finger protein 207
40727_at	down	0.047283047	anaphase-promoting complex subunit 10
38593_r_at	up	0.047357278	KIAA0284 protein
2010_at	down	0.047362414	S-phase kinase-associated protein 1A (p19A)
35575_f_at	up	0.047365962	zinc finger protein 253
1910_s_at	up	0.04741841	B-cell CLL/lymphoma 2
184_at	up	0.047445638	angiotensin II receptor-like 1
38461_at	up	0.04746726	nebulin
38997_at	up	0.047512317	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1
38449_at	up	0.047540057	WD repeat domain 23
36511_at	down	0.047649025	SAC1 suppressor of actin mutations 1-like (yeast)
39660_at	up	0.047681544	defensin, beta 1
1134_at	up	0.04771627	activated p21cdc42Hs kinase
350_at	down	0.047748166	zinc finger protein 161
38108_at	up	0.047777085	palmitoyl-protein thioesterase 2
41572_r_at	down	0.047800461	v-rel reticuloendotheliosis viral oncogene homolog (avian)
36430_at	up	0.047801528	adrenomedullin receptor
183_at	up	0.047811102	microtubule-associated protein 2
33424_at	down	0.047825363	ribophorin I

36289_f_at	up	0.047833702	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)
352_at	up	0.047842757	phosphatidylinositol transfer protein
37481_at	down	0.047846427	cell division cycle 40 homolog (yeast)
38671_at	up	0.04786849	plexin D1
36421_at	up	0.04790502	
40687_at	up	0.047916691	gap junction protein, alpha 4, 37kDa (connexin 37)
33903_at	up	0.047941918	death-associated protein kinase 3
40002_r_at	up	0.048072194	chorea acanthocytosis
33309_at	down	0.048101663	comparative gene identification 58
40831_at	down	0.048137628	DKFZP586B0923 protein
35907_at	up	0.048159735	cyclin F
494_at	up	0.048164571	interleukin 13
32112_s_at	down	0.048170984	absent in melanoma 1
34253_at	down	0.048212712	nucleoporin 160kDa
36998_s_at	down	0.048223756	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)
34217_at	up	0.048263151	Kruppel-like factor 7 (ubiquitous)
671_at	down	0.048295042	secreted protein, acidic, cysteine-rich (osteonectin)
36934_at	down	0.048313588	chromosome 20 open reading frame 111
33589_at	up	0.048381236	
34811_at	down	0.048384646	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
41420_at	down	0.048387986	insulin-like growth factor binding protein 5
1961_f_at	up	0.048390228	nitric oxide synthase 3 (endothelial cell)
32778_at	down	0.048408	inositol 1,4,5-triphosphate receptor, type 1
1376_at	up	0.048423676	ligase I, DNA, ATP-dependent
31648_at	up	0.048427152	chromosome 6 open reading frame 54
36533_at	up	0.048431505	prostaglandin I2 (prostacyclin) synthase
691_g_at	up	0.048436464	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55)
823_at	up	0.048447199	chemokine (C-X3-C motif) ligand 1
39254_at	up	0.048494182	retinoic acid induced 14
31826_at	up	0.04850013	KIAA0674 protein
35247_at	down	0.048510979	small nuclear RNA activating complex, polypeptide 5, 19kDa
777_at	down	0.048547239	GDP dissociation inhibitor 2



36561_at	down	0.048563389	propionyl Coenzyme A carboxylase, beta polypeptide
32597_at	down	0.048567647	retinoblastoma-like 2 (p130)
39315_at	up	0.048579702	angiopoietin 1
33099_at	up	0.048604195	fucosyltransferase 5 (alpha (1,3) fucosyltransferase)
37383_f_at	up	0.048648959	major histocompatibility complex, class I, C
36479_at	up	0.048655756	growth arrest-specific 8
35804_at	down	0.04866351	ash2 (absent, small, or homeotic)-like (Drosophila)
39258_at	down	0.048682346	ring finger protein 126
31560_at	up	0.04868959	interleukin 1 receptor-like 2
34694_at	up	0.048706288	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
37398_at	down	0.04874917	platelet/endothelial cell adhesion molecule (CD31 antigen)
33701_at	up	0.048783164	phenylalanine hydroxylase
40338_at	up	0.048799432	
38047_at	up	0.048809968	RNA binding protein with multiple splicing
1552_l_at	up	0.048820655	cytochrome P450, family 2, subfamily A, polypeptide 13
32997_at	up	0.04888841	G antigen, family B, 1 (prostate associated)
33506_at	up	0.048920322	inositol polyphosphate-4-phosphatase, type I, 107kDa
36257_at	up	0.049004519	
896_at	up	0.049060786	mucin 2, intestinal/tracheal
37101_at	up	0.049085465	breast cancer metastasis-suppressor 1
37612_at	up	0.049087566	parvalbumin
33636_at	up	0.0490977	cancer/testis antigen 1
31349_at	up	0.049121601	DNA-binding protein amplifying expression of surfactant protein B
39624_at	up	0.049180262	leukotriene B4 receptor
33327_at	up	0.04919815	chromosome 11 open reading frame 9
33952_at	up	0.049220745	zinc finger protein 306
34631_at	up	0.04924553	eyes absent homolog 4 (Drosophila)
33890_at	up	0.049248261	regulator of G-protein signalling 5
33646_g_at	up	0.049269594	GM2 ganglioside activator protein
39065_s_at	down	0.049283287	tetratricopeptide repeat domain 3
32783_at	up	0.049303682	fibulin 2
35843_at	down	0.049309055	NIMA (never in mitosis gene a)- related kinase 9
41613_at	up	0.04933168	KIAA0329 gene product
33912_at	down	0.049387377	zinc metalloproteinase (STE24 homolog, yeast)

34093_at	up	0.049407315	
32772_s_at	up	0.049413791	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1
34402_at	down	0.049425825	unr-interacting protein
39372_at	down	0.049477707	fatty acid desaturase 1
1254_at	up	0.04948114	guanylate cyclase activator 1A (retina)
36121_at	up	0.049509564	epsin 2
33011_at	up	0.049521701	neurotensin receptor 2
37732_at	down	0.049539909	RING1 and YY1 binding protein
36863_at	up	0.049676408	hyaluronan-mediated motility receptor (RHAMM)
36010_at	up	0.049689666	mesenchyme homeo box 1
38355_at	down	0.049749088	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome
41594_at	down	0.049757578	Janus kinase 1 (a protein tyrosine kinase)
37538_at	up	0.049804213	
41864_at	up	0.04983549	
447_g_at	down	0.0498497	casein kinase 1, gamma 2
1647_at	down	0.049914966	IQ motif containing GTPase activating protein 2
38666_at	down	0.050017281	pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)
37074_at	up	0.05006693	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basi component 1)
38753_at	down	0.050071335	exportin, tRNA (nuclear export receptor for tRNAs)
37460_at	up	0.050130808	T-cell lymphoma invasion and metastasis 1
32924_at	up	0.050139399	matrix metalloproteinase 24 (membrane-inserted)
33939_at	up	0.05014943	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)
35942_at	up	0.050154516	
41775_at	up	0.050197141	isoprenylcysteine carboxyl methyltransferase
35200_at	up	0.050298469	high mobility group AT-hook 2
34889_at	down	0.050400452	ATPase, H <sup>+</sup> transporting, lysosomal 70kDa, V1 subunit A
40927_at	up	0.050411621	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
1170_at	up	0.050472551	
34647_at	down	0.050512762	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kDa)
595_at	down	0.050514625	tumor necrosis factor, alpha-induced protein 3
513_at	up	0.050548181	mitogen-activated protein kinase kinase 5

36567_at	up	0.05061091	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7
35386_at	up	0.050611701	acetylcholinesterase (YT blood group)
34103_at	up	0.050662538	carboxyl ester lipase (bile salt-stimulated lipase)
39176_f_at	up	0.050705598	
34078_s_at	up	0.050714993	cytochrome P450, family 2, subfamily C, polypeptide 19
362_at	up	0.050721464	protein kinase C, zeta
31341_at	up	0.05078886	potassium voltage-gated channel, Shaw-related subfamily, member 3
140_s_at	down	0.050824342	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
38486_at	up	0.050860569	troponin I, skeletal, slow
40607_at	down	0.050870068	dihydropyrimidinase-like 2
41563_at	up	0.050883454	transient receptor potential cation channel, subfamily M, member 1
38771_at	down	0.050919217	histone deacetylase 1
36514_at	down	0.050919704	cell growth regulatory with ring finger domain
1689_at	up	0.050938547	protocadherin 16 dachshous-like (Drosophila)
33287_at	up	0.051003471	hypothetical protein HSPC109
334_s_at	up	0.051007767	pregnancy specific beta-1-glycoprotein 7
35956_s_at	up	0.05102897	
39704_s_at	down	0.051031896	high mobility group AT-hook 1
885_g_at	up	0.051041395	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
35530_f_at	up	0.051160162	immunoglobulin lambda locus
33458_r_at	down	0.051179962	histone 1, H2bc
1330_at	up	0.051206939	mitogen-activated protein kinase kinase kinase 3
35178_at	up	0.051239142	WNT inhibitory factor 1
36556_at	up	0.051298489	KIAA0672 gene product
34124_at	up	0.051343537	mitochondrial translational release factor 1-like
32869_at	up	0.051360804	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
38527_at	down	0.051367943	non-POU domain containing, octamer-binding
38568_at	down	0.051403125	tumor protein p53-binding protein
39023_at	down	0.051454387	isocitrate dehydrogenase 1 (NADP+), soluble
41650_at	up	0.051471647	WD40 protein C1a01
32582_at	up	0.051507501	myosin, heavy polypeptide 11, smooth muscle

33350_s_at	down	0.051519969	JM5 protein
36098_at	down	0.051540433	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
35499_at	up	0.051549928	hypothetical protein FLJ11336
31584_at	down	0.051651619	tumor protein, translationally-controlled 1
33660_at	down	0.051688017	ribosomal protein L5
36895_at	down	0.051724914	origin recognition complex, subunit 3-like (yeast)
33228_g_at	down	0.051742066	interleukin 10 receptor, beta
31752_at	up	0.051948954	hypothetical protein FLJ23142
418_at	up	0.051966256	antigen identified by monoclonal antibody Ki-67
39401_at	up	0.052038202	ribosomal protein S13
1343_s_at	up	0.052108915	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3
855_at	down	0.052145184	programmed cell death 2
1174_at	up	0.052217952	
37152_at	down	0.052254523	peroxisome proliferative activated receptor, delta
37931_at	up	0.052279349	centromere protein B, 80kDa
41530_at	down	0.052346679	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)
1859_s_at	up	0.05236121	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)
35975_at	down	0.052380431	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3
33101_g_at	up	0.052389477	fetuin B
1974_s_at	up	0.052421103	tumor protein p53 (Li-Fraumeni syndrome)
1280_i_at	up	0.052503614	
38600_r_at	up	0.052520183	
35426_at	up	0.052533016	SPPL2b
31978_at	up	0.052541422	kinesin family member 25
38746_at	up	0.052620875	integrin, beta 4
41153_f_at	down	0.052679177	catenin (cadherin-associated protein), alpha 1, 102kDa
35812_at	up	0.052688828	transportin-SR
40788_at	up	0.052750269	adenylate kinase 2
40324_r_at	up	0.052791746	topoisomerase (DNA) III beta
35271_at	down	0.052803954	ARP3 actin-related protein 3 homolog (yeast)

38910_at	up	0.052829015	ATP synthase mitochondrial F1 complex assembly factor 2
38095_i_at	down	0.052863898	major histocompatibility complex, class II, DP beta 1
35267_g_at	down	0.052865754	bladder cancer associated protein
38945_at	up	0.052875372	metal-regulatory transcription factor 1
38522_s_at	down	0.052897744	CD22 antigen
31567_at	up	0.052906998	gamma-aminobutyric acid (GABA) A receptor, gamma 3
37099_at	down	0.052981643	arachidonate 5-lipoxygenase-activating protein
562_g_at	up	0.053109055	follicle stimulating hormone receptor
33906_at	up	0.053130467	Sjogren's syndrome/scleroderma autoantigen 1
40846_g_at	down	0.053163872	interleukin enhancer binding factor 3, 90kDa
34312_at	down	0.053202442	nuclear receptor coactivator 2
38644_at	up	0.053219276	paxillin
33834_at	up	0.053224091	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
155_s_at	down	0.053379913	ubiquitin-like 1 (sentrin)
31363_at	up	0.053396497	CCR4-NOT transcription complex, subunit 2
32966_at	up	0.053413878	apolipoprotein F
35227_at	up	0.053429325	retinoblastoma binding protein 8
1537_at	up	0.053442744	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
32122_at	up	0.053448125	sulfite oxidase
35515_at	up	0.053507235	tektin 2 (testicular)
40387_at	down	0.053544896	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
1718_at	down	0.053617875	actin related protein 2/3 complex, subunit 2, 34kDa
33341_at	down	0.053655896	guanine nucleotide binding protein (G protein), beta polypeptide 1
40269_at	down	0.053675027	PRP18 pre-mRNA processing factor 18 homolog (yeast)
37000_at	down	0.053751225	DKFZP564B167 protein
1667_s_at	up	0.053766642	cytochrome P450, family 4, subfamily B, polypeptide 1
37993_at	up	0.053772854	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, delta subunit
40883_at	up	0.053801821	syntaxin 16
31420_at	up	0.053822167	immunoglobulin lambda variable (IV)/OR22-1
37980_at	down	0.053851354	CBF1 interacting corepressor

1451_s_at	up	0.05389717	osteoblast specific factor 2 (fasciclin I-like)
39118_at	down	0.05391293	DnaJ (Hsp40) homolog, subfamily A, member 1
39265_at	up	0.053944254	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
34569_at	up	0.053973736	SRY (sex determining region Y)-box 11
1609_g_at	up	0.054005608	
35168_f_at	down	0.054037696	collagen, type XVI, alpha 1
40015_at	up	0.054067609	KIAA0303 protein
36219_at	down	0.054111813	similar to Caenorhabditis elegans protein C42C1.9
33068_f_at	up	0.054171933	UDP glycosyltransferase 2 family, polypeptide B15
538_at	up	0.054185653	CD34 antigen
39503_s_at	up	0.054254903	dihydropyrimidinase-like 4
38427_at	up	0.054256236	collagen, type XV, alpha 1
33448_at	up	0.05426235	serine protease inhibitor, Kunitz type 1
36870_at	down	0.054274318	KIAA0804 protein
41680_at	up	0.054307826	chromosome 1 open reading frame 34
38463_s_at	down	0.054344711	adenosine monophosphate deaminase (isoform E)
36362_at	up	0.054379239	solute carrier family 12 (sodium/chloride transporters), member 3
32704_at	down	0.054445472	dedicator of cyto-kinesis 2
39168_at	up	0.054468601	Ac-like transposable element
40587_s_at	down	0.054472775	eukaryotic translation elongation factor 1 epsilon 1
37081_at	up	0.054493153	dynein, axonemal, heavy polypeptide 7
33447_at	down	0.05449949	myosin regulatory light chain MRCL3
33205_at	up	0.054582892	suppressor of Ty 3 homolog (S. cerevisiae)
41462_at	down	0.054609547	sorting nexin 2
41625_at	down	0.054610798	thyroid hormone receptor-associated protein, 240 kDa subunit
32175_at	down	0.054611527	CDC10 cell division cycle 10 homolog (S. cerevisiae)
36099_at	down	0.054636307	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)
39349_at	up	0.054649873	HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae)
38367_s_at	up	0.054689416	complement component 4 binding protein, beta

1474_s_at	up	0.054758106	v-myb myeloblastosis viral oncogene homolog (avian)
40429_r_at	up	0.054807695	
40502_r_at	up	0.054812914	myosin binding protein C, slow type
34232_at	up	0.054826808	natural killer-tumor recognition sequence
36148_at	up	0.054862015	amyloid beta (A4) precursor-like protein 1
1040_s_at	up	0.054877884	abl-interactor 2
41692_at	down	0.054891324	synaptojanin 1
32569_at	down	0.054893855	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa
160030_at	up	0.054898491	growth hormone receptor
32452_at	up	0.054953745	cyclin-dependent kinase 3
36639_at	up	0.054982119	adenylosuccinate lyase
40357_at	up	0.054984105	inhibin, beta A (activin A, activin AB alpha polypeptide)
31437_r_at	up	0.05500989	estrogen receptor 2 (ER beta)
38802_at	down	0.055010478	progesterone receptor membrane component 1
41837_at	up	0.055099827	chromosome 14 open reading frame 132
261_s_at	up	0.055127541	apolipoprotein B (including Ag(x) antigen)
38083_at	down	0.0551325	Notch homolog 2 (Drosophila)
35611_at	up	0.055135445	zinc finger protein 37 homolog (mouse)
41812_s_at	down	0.055143341	nucleoporin 210
37535_at	down	0.055180046	cAMP responsive element binding protein 1
38800_at	up	0.05524435	stathmin-like 2
41663_at	up	0.0552624	
36575_at	up	0.055284709	regulator of G-protein signalling 1
39739_at	down	0.055289363	nascent-polypeptide-associated complex alpha polypeptide
38562_g_at	up	0.055320447	down-regulated in metastasis
41052_s_at	up	0.055330253	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
39548_at	up	0.055386674	neuronal PAS domain protein 2
31929_at	down	0.055389172	regulatory factor X, 3 (influences HLA class II expression)
1946_at	up	0.055451877	Wilms tumor associated protein

32324_at	down	0.055453311	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
38660_at	up	0.055562135	cytochrome c oxidase subunit VIa polypeptide 2
38370_at	down	0.055580846	trophinin associated protein (tastin) proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional protease 7)
32702_at	up	0.055632752	
41184_s_at	down	0.055648432	
33542_at	up	0.05569065	chromosome X open reading frame 1 eukaryotic translation elongation factor 1 gamma
34444_at	up	0.055727944	
33043_at	up	0.055762089	
34461_at	up	0.055819194	synaptonemal complex protein 1
40243_at	up	0.055858811	metallo phosphoesterase
36599_at	down	0.055883675	malic enzyme 2, NAD(+)-dependent, mitochondrial
32026_s_at	down	0.055895289	PDZ domain containing guanine nucleotide exchange factor (GEF 1
33272_at	up	0.055916736	serum amyloid A1
35412_at	up	0.055920677	cytochrome P450, family 4, subfamily A, polypeptide 11
31753_at	up	0.056077168	lipidosin ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)
32537_at	up	0.05609059	
36411_s_at	up	0.056166675	
31844_at	down	0.056320576	homogentisate 1,2-dioxygenase (homogentisate oxidase)
530_at	up	0.056385304	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2
903_at	down	0.056390908	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
39283_at	up	0.056439846	apical protein-like (Xenopus laevis) prostaglandin D2 synthase 21kDa (brain)
38406_f_at	up	0.05649877	
39239_at	up	0.056512111	CD8 antigen, beta polypeptide 1 (p37)
32481_at	up	0.056673095	sorting nexin 7 septin 6
37808_at	up	0.056785668	
37775_at	up	0.056808833	
938_at	up	0.056826365	KIAA0420 gene product N-myc (and STAT) interactor proteasome (prosome, macropain) subunit, beta type, 4
34921_at	up	0.056875557	
36472_at	down	0.056888332	
33154_at	down	0.05689138	
41173_at	up	0.05691759	REST corepressor transformer-2 alpha (htra-2 alpha)
37651_at	down	0.056919669	
39344_at	down	0.056934629	



1548_s_at	up	0.056952857	interleukin 10
34574_at	up	0.056969408	melanoma antigen, family A, 11
36493_at	down	0.056992416	lymphocyte-specific protein 1
41243_at	down	0.057169482	solute carrier family 35, member E2
34446_at	down	0.057273151	KIAA0471 gene product
37595_at	up	0.057288566	
40317_at	up	0.057307104	amiloride-sensitive cation channel 1, neuronal (degenerin)
1948_f_at	up	0.057328317	nitric oxide synthase 2A (inducible, hepatocytes)
39973_at	up	0.057344468	leprecan-like 2 protein
40785_g_at	down	0.057345337	protein phosphatase 2, regulatory subunit B (B56), gamma isoform
32076_at	up	0.057364647	Down syndrome critical region gene 1-like 1
35514_at	up	0.057373421	Rho family guanine-nucleotide exchange factor
41152_f_at	down	0.057442439	ribosomal protein L36a
38395_at	down	0.057443145	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
160042_s_at	up	0.057472079	homeo box B6
388_at	up	0.057530222	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85. beta)
41214_at	down	0.057534645	ribosomal protein S4, Y-linked
35969_at	up	0.057696203	M-phase phosphoprotein 9
38023_at	up	0.057706011	phosphatidylinositol transfer protein
39306_at	up	0.057708653	protease, serine, 16 (thymus)
33246_at	up	0.057726548	mitogen-activated protein kinase 13
32809_at	down	0.057746743	
37862_at	up	0.057768456	dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease)
1886_at	up	0.057823252	wingless-type MMTV integration site family, member 7A
36519_at	down	0.057885294	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
36465_at	up	0.058006837	interferon regulatory factor 5
1236_s_at	up	0.058010665	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)
38299_at	up	0.058034422	interleukin 6 (interferon, beta 2)
35928_at	up	0.058057431	thyroid peroxidase
32029_at	up	0.058077367	3-phosphoinositide dependent protein kinase-1

36104_at	down	0.058084978	ubiquinol-cytochrome c reductase hinge protein
37893_at	down	0.05809969	protein tyrosine phosphatase, non-receptor type 2
713_at	up	0.05811789	
32918_at	up	0.058151217	
37917_at	down	0.05818336	hypothetical protein FLJ20323
1788_s_at	up	0.058232158	dual specificity phosphatase 4
31769_at	up	0.058233033	wingless-type MMTV integration site family, member 8B
39219_at	down	0.058252593	CCAAT/enhancer binding protein (C/EBP), gamma
416_s_at	up	0.058290651	homeo box C5
33457_at	down	0.058377788	retinoblastoma-associated protein 140
37718_at	down	0.058387995	SNF-1 related kinase
34053_at	up	0.058414295	zona pellucida binding protein
38245_i_at	up	0.058439157	mitogen-activated protein kinase kinase kinase kinase 5
37943_at	down	0.05843963	zinc finger, FYVE domain containing 26
40401_at	up	0.058454018	docking protein 5
39048_at	up	0.0585224	Notch homolog 4 (Drosophila)
41023_at	up	0.058574201	complement component 8, alpha polypeptide
37824_at	up	0.058584019	KIAA1074 protein
39819_at	up	0.058650541	RNA polymerase I transcription factor RRN3
41231_f_at	down	0.058672904	high-mobility group nucleosomal binding domain 2
682_at	up	0.058711408	interferon, alpha 8
38931_at	down	0.058759428	zinc finger protein, X-linked
40509_at	down	0.058761269	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)
32306_g_at	up	0.058783564	collagen, type I, alpha 2
38223_at	down	0.058796236	TBC1 domain family, member 8 (with GRAM domain)
37920_at	up	0.058825806	paired-like homeodomain transcription factor 1
41821_at	down	0.05885646	cell division cycle 2-like 5 (cholinesterase-related cell division controller)
40575_at	up	0.058887769	discs, large (Drosophila) homolog 5
33714_at	up	0.058937876	high-mobility group box 3
36778_at	down	0.059000095	ocular albinism 1 (Nettleship-Falls)
369_s_at	up	0.059042852	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
34612_at	up	0.05904774	calbindin 3, (vitamin D-dependent calcium binding protein)
38364_at	down	0.059052258	B lymphocyte gene 1

40952_at	up	0.059083867	BTG3 associated nuclear protein
1008_f_at	up	0.059087627	protein kinase, Interferon-inducible double stranded RNA dependent
38930_at	up	0.059243009	
37568_at	up	0.059295057	
40011_s_at	up	0.059317671	fragile X mental retardation 2
34482_at	down	0.059336699	hypothetical protein MGC4701
38620_at	up	0.059347346	golgi SNAP receptor complex member 2
32641_at	down	0.059370035	androgen-induced proliferation inhibitor
41848_f_at	up	0.059393969	interleukin 24
1446_at	down	0.059425354	proteasome (prosome, macropain) subunit, alpha type, 2
1611_s_at	up	0.059473457	interferon, gamma
34519_at	up	0.05950626	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
34792_at	down	0.059523377	S-adenosylhomocysteine hydrolase-like 1
1787_at	down	0.05953562	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
36975_at	down	0.059558803	hypothetical protein MGC8721
34337_s_at	down	0.05957962	likely ortholog of mouse metal response element binding transcription factor 2
39491_s_at	up	0.059588745	
37623_at	up	0.059601491	nuclear receptor subfamily 4, group A, member 2
37483_at	down	0.059686507	histone deacetylase 9
937_at	down	0.059741003	
32168_s_at	down	0.059758424	Down syndrome critical region gene 1
37524_at	down	0.059785317	serine/threonine kinase 17b (apoptosis-inducing)
31776_at	up	0.059797735	
37590_g_at	up	0.059839604	
1113_at	up	0.060099594	bone morphogenetic protein 2
34595_at	up	0.060161002	myosin IA
40608_at	down	0.060169789	ribosomal protein S13
36935_at	down	0.060188988	RAS p21 protein activator (GTPase activating protein) 1
32246_g_at	down	0.060205029	chromosome 14 open reading frame 92
34891_at	down	0.060240172	dynein, cytoplasmic, light polypeptide 1

40337_at	up	0.060277334	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)
35326_at	up	0.060313969	Ylp1 interacting factor homolog (S. cerevisiae)
38983_at	down	0.060318989	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
38783_at	up	0.060335185	mucin 1, transmembrane
36597_at	down	0.060379177	nucleolar and colled-body phosphoprotein 1
1445_at	up	0.060466022	chemokine (C-C motif) receptor-like 2
40212_at	up	0.06048741	kinase suppressor of ras
1057_at	up	0.060533082	cellular retinoic acid binding protein 2
35992_at	up	0.060585199	musculin (activated B-cell factor-1)
40084_at	down	0.060604175	transcription factor CP2
38685_at	down	0.060642908	syntaxin 12
35089_at	up	0.060731492	neuregulin 2
38672_at	up	0.060809774	protein phosphatase 1, regulatory subunit 10
38454_g_at	down	0.060868973	intercellular adhesion molecule 2
34208_at	up	0.060876759	solute carrier family 12, (potassium-chloride transporter) member 5
39278_at	up	0.060889133	transglutaminase 4 (prostate)
37581_at	down	0.060941394	protein phosphatase 6, catalytic subunit
38442_at	up	0.060971291	microfibrillar-associated protein 2
37634_at	up	0.060996525	progesterone-associated endometrial protein (placental protein 14 pregnancy-associated endometrial alpha-2-globulin, alpha uterine protein)
729_i_at	up	0.061028761	
33402_at	up	0.061073887	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
41824_at	down	0.061082771	CGI-48 protein
35377_at	up	0.061238393	DKFZP434M154 protein
39205_at	up	0.061272223	hypothetical protein PP1665
584_s_at	down	0.061289672	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)
38261_at	down	0.061331903	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
40937_at	up	0.061382943	zinc finger protein 291
33376_at	up	0.061386605	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1
39571_at	up	0.0614091	hypothetical protein DKFZp434G2311
36670_at	up	0.061452772	autoantigen

31675_s_at	down	0.06149695	phosphatase and tensin homolog (mutated in multiple advanced cancers 1), pseudogene 1
34730_g_at	up	0.061538175	trophinin
41556_s_at	up	0.061577406	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
35737_at	up	0.061613514	high mobility group nucleosomal binding domain 4
36064_at	up	0.061678211	potassium voltage-gated channel, KQT-like subfamily, member 2
34829_at	up	0.061682903	dyskeratosis congenita 1, dyskerin
1592_at	up	0.061762496	topoisomerase (DNA) II alpha 170kDa
34657_at	down	0.06176476	A kinase (PRKA) anchor protein 11
33254_at	down	0.061846647	ecotropic viral integration site 5
1367_f_at	down	0.061855363	ubiquitin C
38060_at	down	0.061883861	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
33797_at	up	0.06191586	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
35294_at	down	0.061934664	Sjogren syndrome antigen A2 (60kDa, ribonucleoprotein autoantigen SS-A/Ro)
39437_at	up	0.061948929	zinc finger protein 289, ID1 regulated
34723_at	down	0.061958734	COX11 homolog, cytochrome c oxidase assembly protein (yeast)
40800_at	up	0.061977237	HN1 like
40300_g_at	up	0.062012415	G-protein coupled receptor
2013_at	up	0.062019318	transcription factor Dp-2 (E2F dimerization partner 2)
398_at	up	0.062027909	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated)
35700_at	up	0.062054825	chromodomain helicase DNA binding protein 2
37176_at	up	0.0620627	hyaluronoglucosaminidase 1
35906_at	up	0.062070421	solute carrier family 5 (sodium/glucose cotransporter), member 1
38306_at	down	0.062100311	brefeldin A-inhibited guanine nucleotide-exchange protein 1
33943_at	down	0.062127606	ferritin, heavy polypeptide 1
31652_at	up	0.062177255	KIAA1000 protein
39115_at	down	0.06219621	cysteine-rich with EGF-like domains 1
1897_at	up	0.062201284	transforming growth factor, beta receptor III (betaglycan, 300kDa)
288_s_at	down	0.062457541	lamin B receptor
904_s_at	up	0.06249421	topoisomerase (DNA) II alpha 170kDa

34544_at	down	0.06257331	zinc finger protein 267
38622_at	up	0.062579122	hypothetical protein BC004409
32099_at	down	0.062599116	scaffold attachment factor B2
33485_at	down	0.062675228	ribosomal protein L4
38778_at	down	0.062677106	KIAA1046 protein
966_at	up	0.0627393	RAD54-like ( <i>S. cerevisiae</i> )
34111_s_at	up	0.062792399	
35272_at	down	0.062795602	guanine nucleotide binding protein (G protein), gamma 5
32807_at	down	0.062914078	DKFZP566C134 protein
37913_at	up	0.062920328	dihydrofolate reductase
36226_r_at	up	0.062926066	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
39885_at	down	0.062939041	putative dimethyladenosine transferase
34571_at	up	0.063007099	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2
39602_at	up	0.063009221	myosin VIIA and Rab interacting protein
34594_at	down	0.063034238	related to the N terminus of tre
40809_at	up	0.063035272	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basi component 2)
40707_at	up	0.06310375	M-phase phosphoprotein 9
33684_at	up	0.0631076	wingless-type MMTV integration site family, member 2B
31973_at	up	0.063114368	calcium channel, voltage-dependent, alpha 1G subunit
32382_at	up	0.063143488	uroplakin 1B
102_at	up	0.0632572	homeodomain interacting protein kinase 3
38818_at	down	0.063335303	serine palmitoyltransferase, long chain base subunit 1
32549_at	up	0.063359153	pregnancy-associated plasma protein A
32780_at	up	0.063441097	bullous pemphigoid antigen 1, 230/240kDa
37586_at	up	0.063463781	zinc finger protein 142 (clone pHZ-49)
31728_at	up	0.063480732	major histocompatibility complex, class II, DO alpha
33324_s_at	up	0.063481517	cell division cycle 2, G1 to S and G2 to M
33722_at	down	0.063552526	attractin
31618_at	up	0.063629282	
37231_at	up	0.063647129	discs, large homolog 7 ( <i>Drosophila</i> )
33295_at	up	0.063653906	Duffy blood group
38344_at	down	0.0636827	Alstrom syndrome 1
630_at	up	0.063683304	dCMP deaminase
39828_at	up	0.063688282	ADP-ribosylation factor-like 7

36932_at	down	0.063720811	general transcription factor IIIC, polypeptide 2, beta 110kDa
1213_at	down	0.063729631	SFRS protein kinase 2
36757_at	down	0.063735666	histone 1, H3h
41856_at	up	0.063822614	
40717_at	up	0.063953051	cathepsin L2
37142_at	up	0.064046062	GDNF family receptor alpha 1
34772_at	up	0.064054956	coronin, actin binding protein, 2B
36060_at	down	0.064069461	signal recognition particle 54kDa
1291_s_at	up	0.064069798	fibroblast growth factor receptor 4
40029_at	up	0.064078515	EGF-like-domain, multiple 3
37072_at	up	0.064097818	cyclic nucleotide gated channel beta 1
38860_at	up	0.064166427	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)
1490_at	up	0.064176408	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)
38679_g_at	down	0.064193026	small nuclear ribonucleoprotein polypeptide E
31946_s_at	up	0.064273083	forkhead box G1A
38266_at	down	0.064299188	retinoblastoma binding protein 6
33334_at	down	0.064353716	acylphosphatase 1, erythrocyte (common) type
1737_s_at	up	0.064389565	insulin-like growth factor binding protein 4
1781_at	up	0.064434279	ELK1, member of ETS oncogene family
39396_at	down	0.064438229	lysophospholipase I
34063_at	up	0.064446601	RecQ protein-like 5
37230_at	down	0.064472303	KIAA0469 gene product
32265_at	up	0.064485263	nuclear receptor subfamily 4, group A, member 1
40832_s_at	down	0.064506377	lamina-associated polypeptide 1B
35356_at	down	0.064514009	hypothetical protein MGC9651
40539_at	up	0.064543391	myosin IXB
40984_at	up	0.064566113	gamma tubulin ring complex protein (76p gene)
41376_i_at	up	0.064571434	UDP glycosyltransferase 2 family, polypeptide B7
41576_at	up	0.064620473	
273_g_at	up	0.064629736	gastrin-releasing peptide
37022_at	up	0.064629783	proline arginine-rich end leucine-rich repeat protein
722_at	up	0.06464731	RCD1 required for cell differentiation1 homolog (S. pombe)
34077_at	up	0.064651773	chemokine (C-X-C motif) receptor 3
37341_at	up	0.064654132	glutamate dehydrogenase 1

39481_at	up	0.06467974	long-chain fatty-acyl elongase
36436_at	up	0.064760378	leukocyte cell-derived chemotaxin 2
35716_at	up	0.064783583	sulfotransferase family, cytosolic, 1C, member 1
133_at	down	0.064821382	cathepsin C
36312_at	down	0.064882797	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8
41000_at	down	0.064912113	checkpoint suppressor 1
31677_at	up	0.064958769	
1528_at	up	0.06500764	hypothetical gene CG030
36864_at	up	0.065008406	peroxisomal biogenesis factor 3
36325_at	up	0.065037727	crystallin, beta A1
33413_at	down	0.065039089	protein tyrosine phosphatase type IVA, member 1
40336_at	up	0.0651239	ferredoxin reductase
41597_s_at	down	0.065192685	SEC22 vesicle trafficking protein-like 1 ( <i>S. cerevisiae</i> )
39536_at	up	0.065201347	homeo box (H6 family) 1
1073_at	down	0.065224227	transcription elongation factor A (SII), 1
39594_f_at	up	0.065236518	metallothionein 1H
32974_at	up	0.065273556	homolog of Yeast RRP4 (ribosomal RNA processing 4), 3'-5'-exoribonuclease
37126_at	up	0.065330653	Sjogren syndrome antigen A1 (52kDa, ribonucleoprotein autoantigen SS-A/Ro)
34693_at	down	0.065343616	sialyltransferase
37925_r_at	up	0.065370621	apolipoprotein M
1190_at	up	0.065390496	protein tyrosine phosphatase, receptor type, O
39243_s_at	down	0.065560845	PC4 and SFRS1 interacting protein 2
40333_at	up	0.065610099	bone morphogenetic protein 4
40428_i_at	up	0.065620187	
35703_at	down	0.065621274	platelet-derived growth factor alpha polypeptide
33754_at	up	0.065631647	thyroid transcription factor 1
36620_at	down	0.065767238	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
40710_at	up	0.065846675	calmegin
38629_at	up	0.065898386	microtubule-associated protein tau
41395_at	up	0.06595199	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1
32489_at	up	0.065955036	glutamate receptor, ionotropic, N-methyl D-aspartate 2B



35022_at	up	0.065980914	SRY (sex determining region Y)-box 5
33861_at	down	0.066186823	CCR4-NOT transcription complex, subunit 2
39394_at	up	0.066198374	MAD, mothers against decapentaplegic homolog 9 (Drosophila)
32986_s_at	up	0.066223752	
1707_g_at	up	0.066240761	v-raf murine sarcoma 3611 viral oncogene homolog 1
35078_at	up	0.066266338	intercellular adhesion molecule 4, Landsteiner-Wiener blood group
32846_s_at	down	0.066279462	kinectin 1 (kinesin receptor)
39615_at	up	0.066293934	KIAA1026 protein
39552_at	down	0.06636328	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
41297_at	up	0.066367138	mannosidase, alpha, class 1A, member 2
36290_s_at	up	0.0663784	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)
33367_s_at	down	0.066406849	ornithine decarboxylase antizyme inhibitor
40536_f_at	up	0.066482666	translation initiation factor IF2
32148_at	up	0.066539346	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
1542_at	up	0.066618173	epidermal growth factor (beta-urogastrone)
31419_r_at	up	0.066633328	
39096_at	down	0.066635074	SON DNA binding protein
34762_at	up	0.066729339	ring finger protein (C3HC4 type) 8
36672_at	down	0.066753245	prolylcarboxypeptidase (angiotensinase C)
39475_at	up	0.066768992	chromosome 4 open reading frame 9
947_at	up	0.066788523	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)
894_g_at	up	0.06685321	ubiquitin carrier protein
34654_at	down	0.066869319	myotubularin related protein 1
36449_s_at	up	0.066888403	peptide YY
40125_at	down	0.066905911	calnexin
39629_at	up	0.066929858	phospholipase A2, group V
40444_s_at	up	0.066945781	catenin (cadherin-associated protein), delta 1
581_at	up	0.066955198	laminin, beta 1
38715_at	up	0.066966094	glycophorin B (includes Ss blood group)

32835_at	down	0.066974462	sudD suppressor of bimD6 homolog (A. nidulans)
39510_r_at	down	0.067021841	programmed cell death 4 (neoplastic transformation inhibitor)
41535_at	down	0.06707185	CDK2-associated protein 1
32667_at	up	0.067095946	collagen, type IV, alpha 5 (Alport syndrome)
31971_at	up	0.067178117	putative GR6 protein
789_at	up	0.067241382	early growth response 1
39636_at	up	0.067253181	
31765_at	up	0.067273333	KIAA0694 gene product
35776_at	up	0.067316705	intersectin 1 (SH3 domain protein)
39125_at	up	0.067337952	transient receptor potential cation channel, subfamily C, member 1
34384_at	down	0.067348878	ATP-binding cassette, sub-family C (CFTR/MRP), member 1
1540_f_at	up	0.067365851	interferon, alpha 5
961_at	up	0.067375409	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)
35069_at	up	0.067384697	hypothetical protein similar to preferentially expressed antigen of melanoma
32754_at	up	0.067393559	tropomyosin 3
33872_at	up	0.067430249	latrophilin 2
701_s_at	up	0.067454963	
32380_at	up	0.067457336	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)
34749_at	down	0.06748559	solute carrier family 31 (copper transporters), member 2
40980_at	up	0.067495072	helicase with SNF2 domain 1
39327_at	up	0.067577451	Melanoma associated gene
31663_at	up	0.06777859	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4
39148_s_at	up	0.067828539	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
36616_at	down	0.06785433	DAZ associated protein 2
37530_s_at	up	0.067868284	reelin
41091_at	down	0.067977726	fetal Alzheimer antigen
35064_at	up	0.067980534	tripartite motif-containing 31
40153_at	down	0.067983399	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
34623_at	up	0.06798768	defensin, alpha 5, Paneth cell-specific
39036_g_at	down	0.068092911	progesterin induced protein
33886_at	down	0.068114085	spectrin SH3 domain binding protein 1

40815_g_at	down	0.068233922	iduronate 2-sulfatase (Hunter syndrome)
1000_at	up	0.068270711	mitogen-activated protein kinase 3
41296_s_at	down	0.068276144	START domain containing 7
38648_at	down	0.06827716	zinc finger protein 384
1994_at	up	0.068310712	activating transcription factor 2
35781_g_at	up	0.068345587	KIAA0657 protein
37235_g_at	up	0.068372273	kininogen
32639_at	up	0.068383912	nucleoporin-like protein 1
41470_at	up	0.068392895	prominin 1
723_s_at	down	0.068462859	
39180_at	down	0.068510684	fusion, derived from t(12;16) malignant liposarcoma
33905_at	down	0.068659685	methyl-CpG binding domain protein 2
38459_g_at	up	0.068816314	cytochrome b-5
36673_at	down	0.068888528	mannose phosphate isomerase
160036_at	up	0.068911333	estrogen-related receptor beta
31660_at	up	0.068977387	DKFZP434A062 protein
38200_at	up	0.069062386	faciogenital dysplasia (Aarskog-Scott syndrome)
33651_at	up	0.069111018	aquaporin 8
842_at	up	0.069200967	protein kinase C binding protein 1
208_at	up	0.069215423	catenin (cadherin-associated protein), alpha 2
37140_s_at	up	0.069281532	ectodermal dysplasia 1, anhidrotic
32418_at	up	0.069291623	phosphodiesterase 1C, calmodulin-dependent 70kDa
36214_at	down	0.069400426	Kruppel-like factor 4 (gut)
36685_at	down	0.069578272	adenosylmethionine decarboxylase 1
36311_at	up	0.0696169	phosphodiesterase 1A, calmodulin-dependent
35675_at	up	0.06965234	vinexin beta (SH3-containing adaptor molecule-1)
40162_s_at	up	0.069667733	cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple)
38102_at	down	0.069691466	hypothetical protein FLJ34588
193_at	down	0.069842253	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
32039_at	down	0.069879541	adaptor-related protein complex 3, beta 1 subunit
35604_at	up	0.069916727	endonuclease G-like 1
39346_at	down	0.069917202	KH domain containing, RNA binding, signal transduction associated 1
35844_at	up	0.070023077	syndecan 4 (amphiglycan, ryudocan)

711_at	up	0.070029379	
39378_at	down	0.070031282	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)
2017_s_at	up	0.070139758	cyclin D1 (PRAD1: parathyroid adenomatosis 1)
41361_at	up	0.070337448	CCR4-NOT transcription complex, subunit 8
36387_at	up	0.070387113	
40569_at	up	0.070393476	zinc finger protein 42 (myeloid-specific retinoic acid- responsive)
40489_at	up	0.070419101	dentatorubral-pallidoluysian atrophy (atrophin-1)
37650_at	down	0.070599809	makorin, ring finger protein, 1
1798_at	down	0.07062824	LIV-1 protein, estrogen regulated
35881_at	up	0.070726932	
40545_at	down	0.070878906	proline synthetase co-transcribed homolog (bacterial)
41839_at	up	0.0708905	growth arrest-specific 1
32282_at	up	0.070924055	
39210_at	up	0.070930588	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
31558_at	up	0.070984093	Hr44 antigen
34383_at	down	0.070998576	ubiquitin specific protease 1
33179_at	up	0.071011949	protein phosphatase 1, regulatory (inhibitor) subunit 2
36598_s_at	up	0.071022431	inositol polyphosphate phosphatase-like 1
390_at	up	0.071049442	chemokine (C-C motif) receptor 4
33526_at	up	0.071061356	neuropeptide Y receptor Y2
1748_s_at	up	0.071122402	Kruppel-like factor 1 (erythroid)
40835_at	up	0.071138085	metastasis-associated 1-like 1
36669_at	up	0.071169146	FBJ murine osteosarcoma viral oncogene homolog B
33162_at	down	0.071262469	insulin receptor
35039_at	up	0.071324095	KIAA0276 protein
33390_at	up	0.071340473	serine/threonine kinase 17b (apoptosis-inducing)
33044_f_at	up	0.071406367	empty spiracles homolog 1 (Drosophila)
33248_at	up	0.071526167	
37409_at	down	0.07160345	SFRS protein kinase 2
31783_at	down	0.071657185	renin binding protein
41080_at	up	0.071729743	H2A histone family, member B
519_g_at	up	0.071740889	nuclear receptor subfamily 1, group H, member 2
38079_at	up	0.07176621	guanine nucleotide binding protein (G protein), gamma 12
41723_s_at	down	0.071880267	major histocompatibility complex, class II, DR beta 1
37560_at	up	0.0719212	FLJ00133 protein
32867_at	up	0.071922807	choroideremia (Rab escort protein 1)

41803_g_at	up	0.072091533	hypothetical protein FLJ22531
419_at	up	0.072110323	antigen identified by monoclonal antibody Ki-67
39146_at	up	0.07212862	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, <i>S. cerevisiae</i> )
41175_at	down	0.072189347	core-binding factor, beta subunit
34491_at	up	0.072260618	2'-5'-oligoadenylate synthetase-like
36683_at	up	0.072283268	matrix Gla protein
37598_at	down	0.072298575	Ras association (RalGDS/AF-6) domain family 2
37403_at	down	0.072370544	annexin A1
35862_at	up	0.072384347	solute carrier family 15 (H <sup>+</sup> /peptide transporter), member 2
34242_at	up	0.072461287	chromosome 20 open reading frame 194
331_at	up	0.072463612	
41638_at	down	0.072496969	KIAA0073 protein
215_g_at	up	0.072524414	msh homeo box homolog 1 ( <i>Drosophila</i> )
31642_at	up	0.072608877	
36322_at	up	0.072612703	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)
812_at	down	0.07262422	protein phosphatase 1, regulatory (inhibitor) subunit 2
41345_at	up	0.072637402	purine-rich element binding protein A
34940_at	down	0.072766213	
35909_at	up	0.072779379	pleckstrin homology-like domain, family A, member 1
38856_at	up	0.072867435	KIAA1233 protein
37911_at	up	0.072887305	syntaxin 4A (placental)
36373_at	up	0.072953876	zinc finger, X-linked, duplicated A
37751_at	down	0.07295976	KIAA0255 gene product
39733_at	down	0.073064777	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
33337_at	down	0.073072611	degenerative spermatocyte homolog, lipid desaturase ( <i>Drosophila</i> )
35718_at	down	0.07317749	SP110 nuclear body protein
32253_at	down	0.073249284	arginine-glutamic acid dipeptide (RE) repeats
37229_at	down	0.07336482	ataxia telangiectasia and Rad3 related
34912_at	up	0.073371211	death-associated protein kinase 2
41008_at	up	0.073394717	KIAA0888 protein
41286_at	up	0.073511778	tumor-associated calcium signal transducer 2
1476_s_at	up	0.073525062	v-myb myeloblastosis viral oncogene homolog (avian)
657_at	up	0.073549188	protocadherin gamma subfamily C, 3

40698_at	down	0.073559018	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)
633_s_at	up	0.073596989	transcription factor Dp-2 (E2F dimerization partner 2)
36006_at	up	0.073614666	SRY (sex determining region Y)-box 12
1930_at	down	0.073728457	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
1123_at	up	0.073740648	growth hormone releasing hormone receptor
33146_at	down	0.073857687	myeloid cell leukemia sequence 1 (BCL2-related)
38575_at	down	0.073876745	mucosa associated lymphoid tissue lymphoma translocation gene 1
36506_at	down	0.073893875	A kinase (PRKA) anchor protein (yotiao) 9
32337_at	down	0.073926169	ribosomal protein L21
37385_at	down	0.073942562	peptidyl-prolyl isomerase G (cyclophilin G)
1585_at	up	0.073949466	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
33811_at	down	0.073960943	cell cycle progression 8 protein
37306_at	down	0.073995502	cytoplasmic FMR1 interacting protein 1
35761_at	down	0.07401577	aminoadipate-semialdehyde dehydrogenase-phosphopantetheiny transferase
39776_at	up	0.074189511	unc-51-like kinase 2 (C. elegans)
41060_at	up	0.07422555	cyclin E1
37676_at	down	0.07427798	phosphodiesterase 8A
31839_at	down	0.074281268	splicing factor 4
34998_at	down	0.074281619	protein arginine N-methyltransferase 3(hnRNP methyltransferase S. cerevisiae)-like 3
2018_at	up	0.074304439	gap junction protein, alpha 1, 43kDa (connexin 43)
41004_at	down	0.074346366	topoisomerase (DNA) III alpha
36571_at	down	0.074361104	topoisomerase (DNA) II beta 180kDa
33249_at	up	0.074378692	nuclear receptor subfamily 3, group C, member 2
34953_i_at	up	0.074406032	phosphodiesterase 5A, cGMP-specific
1708_at	up	0.074445148	mitogen-activated protein kinase 10
32674_at	down	0.074454592	NP220 nuclear protein
1204_at	up	0.07450712	diacylglycerol kinase, gamma 90kDa
AFFX-BioC-3_st	up	0.074577771	
39353_at	down	0.074613199	heat shock 10kDa protein 1 (chaperonin 10)
31863_at	down	0.074748576	KIAA0179 protein

38838_at	up	0.074755593	polymyositis/scleroderma autoantigen 1, 75kDa
36035_at	up	0.074835381	GPAA1P anchor attachment protein 1 homolog (yeast)
40422_at	down	0.074893541	insulin-like growth factor binding protein 2, 36kDa
34987_s_at	down	0.07495392	heterogeneous nuclear ribonucleoprotein A1
36124_at	up	0.074965842	mercaptopyruvate sulfurtransferase
35657_at	up	0.074965943	TAR (HIV) RNA binding protein 2
36849_at	up	0.074984491	PTPL1-associated RhoGAP 1
32182_at	down	0.074998717	serine/threonine kinase 38 like
32758_g_at	down	0.075062841	RAE1 RNA export 1 homolog (S. pombe)
461_at	down	0.075106762	N-acylsphingosine amidohydrolase (acid ceramidase) 1
37175_at	up	0.075116156	serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1
34268_at	down	0.075146357	regulator of G-protein signalling 19
528_at	up	0.075153984	heat shock 27kDa protein 3
36224_g_at	down	0.075175637	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
33194_at	up	0.07528018	RCD1 required for cell differentiation1 homolog (S. pombe)
38990_at	down	0.075291777	F-box only protein 9
901_g_at	up	0.075464454	phospholipase C, beta 4
37962_r_at	down	0.07548297	syntaxin binding protein 3
34445_at	down	0.075645748	KIAA0471 gene product
40051_at	up	0.075647797	translocation associated membrane protein 2
34391_at	down	0.07567032	immunoglobulin (CD79A) binding protein 1
40151_s_at	down	0.075685419	peroxisome receptor 1
32183_at	down	0.075709577	splicing factor, arginine/serine-rich 11
40024_at	up	0.075728682	src homology three (SH3) and cysteine rich domain
34611_at	up	0.075745185	zinc finger protein 192
35590_s_at	up	0.075756397	gastric inhibitory polypeptide receptor
38637_at	up	0.075790154	lysyl oxidase
36114_r_at	up	0.07582013	troponin T1, skeletal, slow
39017_at	down	0.075913788	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)
40947_at	up	0.075914155	hypothetical protein FLJ12671
39782_at	down	0.075915309	nuclear DNA-binding protein
1845_at	down	0.075997345	mitogen-activated protein kinase kinase 4

36145_at	up	0.076021749	fuse-binding protein-interacting repressor
32958_at	down	0.076024781	G protein-coupled receptor, family C, group 5, member B
41131_f_at	down	0.076033961	heterogeneous nuclear ribonucleoprotein H2 (H')
40516_at	down	0.076092957	aryl hydrocarbon receptor
35161_at	up	0.07609887	likely ortholog of mouse ubiquitin conjugating enzyme 7 interacting protein 5
38656_s_at	down	0.076198725	hypothetical protein MGC5576
34869_at	up	0.076217032	LIM domain binding 3
40982_at	down	0.076234385	hypothetical protein FLJ10534
36364_at	up	0.07623929	4-aminobutyrate aminotransferase
35751_at	down	0.076289997	succinate dehydrogenase complex, subunit B, iron sulfur (lp)
34907_at	up	0.076316825	apoptosis-associated tyrosine kinase
33111_at	up	0.076325246	natural killer cell receptor, immunoglobulin superfamily member
1500_at	up	0.076347224	Wilms tumor 1
41155_at	down	0.076354576	catenin (cadherin-associated protein), alpha 1, 102kDa
39107_at	up	0.076418762	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
41815_at	down	0.076423878	spectrin repeat containing, nuclear envelope 2
33382_at	down	0.076464267	N-acylsphingosine amidohydrolase (acid ceramidase)-like
690_s_at	up	0.076507955	kinase insert domain receptor (a type III receptor tyrosine kinase)
38699_at	up	0.076517467	tubulin, beta, 5
32315_at	down	0.076580486	ribosomal protein S24
32394_s_at	down	0.076586658	ribosomal protein L23
1323_at	down	0.076619803	ubiquitin B
520_at	up	0.076637949	mitogen-activated protein kinase kinase kinase 12
31977_at	up	0.076645346	guanylate cyclase 2D, membrane (retina-specific)
40874_at	down	0.076645607	endothelial differentiation-related factor 1
41474_at	down	0.076668881	kinesin heavy chain member 2
1508_at	up	0.076750896	integrin, alpha 9
41252_s_at	down	0.07680594	chorionic somatomammotropin hormone 2
35449_at	down	0.076867169	killer cell lectin-like receptor subfamily B, member 1
38478_at	up	0.07688698	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)



33188_at	up	0.076919217	peptidylprolyl isomerase (cyclophilin)-like 2
41753_at	up	0.076936025	actinin, alpha 4
35309_at	up	0.076946588	suppression of tumorigenicity 14 (colon carcinoma, matriptase, epithin)
41586_at	up	0.076953724	fibroblast growth factor 18
33729_at	down	0.076996832	solute carrier family 25 (mitochondrial carrier, brain), member 14
37448_s_at	down	0.07699865	GNAS complex locus
2084_s_at	up	0.077059452	ets variant gene 4 (E1A enhancer binding protein, E1AF)
35118_at	up	0.077061841	lecithin-cholesterol acyltransferase
40327_at	up	0.077082465	homeo box B13
38244_at	up	0.077091148	hypothetical protein FLJ10178
32853_at	down	0.077112143	translocase of outer mitochondrial membrane 70 homolog A (yeast)
38726_at	up	0.077113456	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit
32219_at	down	0.077119778	tousled-like kinase 1
39555_at	down	0.077128151	inhibitor of growth family, member 1-like
35518_at	up	0.07719372	protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle)
39494_at	up	0.07720618	
37023_at	down	0.077401057	lymphocyte cytosolic protein 1 (L-plastin)
41859_at	up	0.077419258	uronyl-2-sulfotransferase
40543_at	up	0.077431976	achaete-scute complex-like 1 (Drosophila)
1232_s_at	up	0.077484241	insulin-like growth factor binding protein 1
41199_s_at	down	0.07749603	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
32300_s_at	up	0.077509791	tyrosine hydroxylase
41546_at	up	0.077594704	cyclin-dependent kinase 6
40044_at	up	0.077618336	ELL gene (11-19 lysine-rich leukemia gene)
34372_at	down	0.077632667	upstream regulatory element binding protein 1
32379_f_at	up	0.07769327	pyruvate kinase, muscle
31475_at	up	0.07772506	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
35322_at	down	0.077745028	Kelch-like ECH-associated protein 1

33741_at	down	0.077773426	ATPase, H <sup>+</sup> transporting, lysosomal 50/57kDa, V1 subunit H
36207_at	down	0.077808208	SEC14-like 1 ( <i>S. cerevisiae</i> )
39504_at	up	0.077809572	gap junction protein, alpha 12, 47kDa
35946_at	up	0.077814129	NEL-like 1 (chicken)
39303_at	up	0.077857901	beta-transducin repeat containing
34946_at	down	0.077936804	immunoglobulin superfamily, member 6
34628_at	up	0.07797503	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa
38045_at	up	0.077978903	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)
38392_at	down	0.077981436	actin related protein 2/3 complex, subunit 5, 16kDa
41825_at	up	0.077994663	PTEN induced putative kinase 1
31333_at	up	0.078003393	tollold-like 1
34686_at	up	0.078059255	adenylate cyclase 2 (brain)
34269_at	down	0.078146471	erythroid differentiation-related factor 1
37725_at	down	0.078156806	protein phosphatase 1, catalytic subunit, gamma isoform
1266_s_at	up	0.078163951	lymphocyte-specific protein tyrosine kinase
1616_at	up	0.078185303	fibroblast growth factor 9 (glia-activating factor)
37563_at	up	0.078201931	SLIT-ROBO Rho GTPase activating protein 2
39336_at	up	0.078228671	ADP-ribosylation factor 3
33698_at	up	0.07823379	KIAA1052 protein
31408_at	up	0.07830084	retinal pigment epithelium-derived rhodopsin homolog
38900_at	up	0.078345513	paired box gene 3 (Waardenburg syndrome 1)
32983_at	up	0.078360832	adrenergic, alpha-1B-, receptor
32252_at	up	0.078369125	transthyretin (prealbumin, amyloidosis type I)
32675_at	down	0.078370483	bone marrow stromal cell antigen 1
1058_at	down	0.07837205	WAS protein family, member 3
34915_at	up	0.078441436	solute carrier family 8 (sodium/calcium exchanger), member 1
41506_at	down	0.078473991	mitogen-activated protein kinase-activated protein kinase 5
160028_s_at	up	0.078607486	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)
1085_s_at	down	0.07863644	phospholipase C, gamma 2 (phosphatidylinositol-specific)

36471_f_at	up	0.078683795	dystrobrevin, alpha
34873_at	up	0.078715546	nebulette
37045_at	down	0.078754743	sorting nexin 19
1682_s_at	up	0.078774726	ATP-binding cassette, sub-family B (MDR/TAP), member 1
557_s_at	up	0.078820073	somatostatin receptor 3
41853_at	down	0.078881429	phosphoribosyl pyrophosphate synthetase-associated protein 2
1207_at	up	0.078910905	cyclin-dependent kinase 6
36228_at	up	0.078961242	glycine-N-acyltransferase
1776_at	up	0.079007645	Ras-related associated with diabetes
39653_at	up	0.079043266	protection of telomeres 1
1652_at	up	0.079084497	pim-2 oncogene
969_s_at	down	0.079111129	ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila)
33847_s_at	down	0.079127006	cyclin-dependent kinase inhibitor 1B (p27, Kip1)
32073_at	down	0.07922512	KIAA0677 gene product
31403_at	up	0.079247982	solute carrier family 18 (vesicular monoamine), member 1
32776_at	down	0.079253268	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)
40585_at	down	0.079269329	adenylate cyclase 7
36696_at	up	0.079410568	phosphatidylinositol glycan, class C, pseudogene 1
1921_at	up	0.079426983	
40377_at	up	0.079435641	KIAA0682 gene product
32916_at	down	0.079476859	protein tyrosine phosphatase, receptor type, E
39444_at	down	0.079505682	splicing factor 3b, subunit 1, 155kDa
32160_at	down	0.079628498	seven in absentia homolog 1 (Drosophila)
33929_at	up	0.079641537	glypican 1
379_at	down	0.079657938	ATP binding protein associated with cell differentiation
31862_at	up	0.07967263	wingless-type MMTV integration site family, member 5A
33027_at	up	0.079685137	
36641_at	down	0.079685686	capping protein (actin filament) muscle Z-line, alpha 2
36703_at	up	0.079773179	chemokine (C-C motif) ligand 25
32447_at	up	0.079824503	nuclear receptor subfamily 5, group A, member 1
39449_at	up	0.079834205	S-phase kinase-associated protein 2 (p45)
39057_at	up	0.079838689	kinesin 2 60/70kDa
32792_at	down	0.07988668	GCIP-interacting protein p29

31461_at	up	0.079924048	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4, pseudogene
38801_at	down	0.079926213	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa
1018_at	up	0.079992699	wingless-type MMTV integration site family, member 10B
37646_at	down	0.079999644	polymerase (DNA directed), delta 3
40093_at	up	0.080005061	Lutheran blood group (Auberger b antigen included)
41855_at	down	0.080076262	histone acetyltransferase 1
40116_at	up	0.080078498	phosphofructokinase, liver
40483_at	up	0.080102456	transcriptional activator of the c-fos promoter
37214_g_at	down	0.080139379	deoxyribonuclease I-like 1
1975_s_at	up	0.080172198	insulin-like growth factor 1 (somatomedin C)
32653_at	up	0.080182256	bromodomain containing 8
33375_at	up	0.080187989	myosin VI
37632_s_at	down	0.080207214	zuotin related factor 1
37353_g_at	down	0.080208739	nuclear antigen Sp100
AFFX-BioB-5_at	up	0.080316663	
34529_at	up	0.080325324	
31459_i_at	up	0.080332933	immunoglobulin lambda locus
35524_at	up	0.080365829	complement component 8, gamma polypeptide
37144_at	up	0.080399764	protein inhibitor of activated STAT protein PIASy
33312_at	down	0.080410486	crystallin, alpha A
37278_at	up	0.080412116	tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndrome)
35973_at	down	0.080418152	huntingtin interacting protein 14
38469_at	up	0.080430213	transmembrane 4 superfamily member 3
35218_at	down	0.080433054	programmed cell death 10
38750_at	up	0.080450803	Notch homolog 3 (Drosophila)
38396_at	up	0.080454362	
37493_at	down	0.080471928	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte macrophage)
38024_at	up	0.080480542	rap2 interacting protein x
34300_at	down	0.080530264	zinc finger protein 278
32367_at	down	0.080576466	signal-regulatory protein beta 1
32504_at	down	0.080592308	sorting nexin 27
1452_at	down	0.080634481	LIM domain only 4

33859_at	down	0.080676216	sin3-associated polypeptide, 18kDa
34462_at	up	0.080685447	sodium channel, nonvoltage-gated 1, delta
34653_at	up	0.080686415	receptor-associated protein of the synapse, 43kD
33466_at	up	0.080709789	hypothetical gene supported by AF038182; BC009203
33880_at	up	0.080756283	fatty-acid-Coenzyme A ligase, long-chain 3
1504_s_at	up	0.080866712	fibroblast growth factor 12
41245_at	up	0.080874178	growth differentiation factor 10
1220_g_at	up	0.080887	interferon regulatory factor 2
38411_at	down	0.080931281	
32017_at	up	0.08094505	par-6 partitioning defective 6 homolog beta (C. elegans)
38581_at	down	0.080999597	guanine nucleotide binding protein (G protein), q polypeptide
32615_at	down	0.081013831	aspartyl-tRNA synthetase
35206_at	up	0.081072588	centrosomal protein 2
2083_at	up	0.081109896	cholecystokinin B receptor
35183_at	up	0.081139697	ATP-binding cassette, sub-family A (ABC1), member 3
39337_at	down	0.081179863	H2A histone family, member Z
32805_at	up	0.081185775	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)
39287_at	up	0.081237036	
35213_at	up	0.081275089	WW domain binding protein 4 (formin binding protein 21)
32090_at	up	0.081301613	nicotinamide nucleotide adenylyltransferase 2
39661_s_at	up	0.081331131	solute carrier family 29 (nucleoside transporters), member 2
41163_at	down	0.081429809	integral type I protein
37382_at	up	0.081475975	ribosomal protein S26
31932_f_at	down	0.0814765	basic transcription factor 3
31354_r_at	up	0.081482365	forkhead box E2
33771_at	up	0.081500647	T-cell activation leucine repeat-rich protein
40994_at	up	0.08156926	G protein-coupled receptor kinase 5
41219_at	down	0.081589471	KIAA0570 gene product
38349_at	down	0.081612444	itchy homolog E3 ubiquitin protein ligase (mouse)
35767_at	down	0.081661911	GABA(A) receptor-associated protein-like 2
1894_f_at	up	0.08166614	

41846_at	up	0.081743099	cone-rod homeobox
38082_at	down	0.081774309	KIAA0650 protein
39581_at	down	0.081796001	cystatin A (stefin A)
38566_at	up	0.081805999	collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia)
35378_at	up	0.081840606	luteinizing hormone beta polypeptide
39788_at	down	0.081846683	plakophilin 4
40358_at	up	0.081926303	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)
35980_at	up	0.081980276	phospholipase C, beta 1 (phosphoinositide-specific)
1790_s_at	up	0.081983581	
35916_s_at	down	0.082014903	heterogeneous nuclear ribonucleoprotein A3
39611_at	up	0.082030651	
32876_s_at	up	0.082062451	rhodopsin (opsin 2, rod pigment) (retinitis pigmentosa 4, autosomal dominant)
35754_at	down	0.082097137	transmembrane trafficking protein
32574_at	up	0.082104017	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)
41565_at	up	0.08210775	ataxin 2 related protein
31340_at	up	0.082177875	matrix metalloproteinase 20 (enamelysin)
219_i_at	up	0.08227682	microtubule-associated protein 2
32968_s_at	up	0.082355877	seizure related 6 homolog (mouse)-like
41212_r_at	down	0.082413942	Williams-Beuren syndrome chromosome region 1
38824_at	down	0.082607893	HIV-1 Tat interactive protein 2, 30kDa
38134_at	down	0.082648743	pleiomorphic adenoma gene 1
1128_s_at	up	0.082677345	chemokine (C-C motif) receptor 1
31393_r_at	up	0.082784321	undifferentiated embryonic cell transcription factor 1
1521_at	down	0.08282553	non-metastatic cells 1, protein (NM23A) expressed in
37523_at	up	0.082918602	acyl-Coenzyme A dehydrogenase, long chain
32244_at	down	0.082923664	chromosome 14 open reading frame 92
38845_at	up	0.082976532	pyruvate dehydrogenase kinase, isoenzyme 2
39759_at	down	0.082990311	quaking homolog, KH domain RNA binding (mouse)
1742_at	up	0.082991136	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
39817_s_at	up	0.083028753	putative c-Myc-responsive

36510_at	down	0.083073712	general transcription factor IIF, polypeptide 2, 30kDa
38087_s_at	down	0.083134517	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)
188_at	up	0.083158625	ephrin-B1
32400_at	up	0.083178012	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1
36753_at	down	0.083213097	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4
37635_at	up	0.083222309	trichohyalin
39268_at	down	0.083225995	potassium voltage-gated channel, subfamily F, member 1
40586_at	up	0.08323434	eukaryotic translation elongation factor 1 epsilon 1
39452_s_at	up	0.083253328	spectrin, beta, non-erythrocytic 1
31563_at	up	0.083296186	
37681_i_at	up	0.083326759	matrin 3
37426_at	up	0.083400663	trinucleotide repeat containing 9
40286_r_at	up	0.08342016	
39524_at	up	0.08346012	rhodopsin (opsin 2, rod pigment) (retinitis pigmentosa 4, autosomal dominant)
1668_s_at	down	0.08347108	von Hippel-Lindau syndrome
835_at	up	0.083523429	PDGFA associated protein 1
37661_at	down	0.083561216	ATPase, Ca++ transporting, plasma membrane 1
35702_at	up	0.083576593	hydroxysteroid (11-beta) dehydrogenase 1
32460_at	up	0.083625268	gamma-aminobutyric acid (GABA) A receptor, beta 2
40732_at	down	0.083646527	nuclear protein, ataxia-telangiectasia locus
32276_at	down	0.083660424	ribosomal protein L32
35652_g_at	down	0.083671345	mitogen-activated protein kinase kinase kinase 4
41429_at	up	0.083680874	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65) beta isoform
33994_g_at	up	0.083688844	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
38284_at	up	0.083709948	myeloid/lymphoid or mixed-lineage leukemia 4
40592_at	up	0.08373631	iduronate 2-sulfatase (Hunter syndrome)

39519_at	down	0.083740037	KIAA0692 protein
37871_at	up	0.083797679	islet amyloid polypeptide
38635_at	down	0.083816871	signal sequence receptor, delta (translocon-associated protein delta)
40246_at	down	0.083844581	discs, large (Drosophila) homolog 1
33948_at	up	0.083864694	corticotropin releasing hormone receptor 2
36087_at	up	0.083865581	KIAA0409 protein
515_s_at	up	0.083916267	Cas-Br-M (murine) ecotropic retroviral transforming sequence b
38948_at	up	0.083927389	protein phosphatase 1, regulatory subunit 3D
32500_at	up	0.083952172	
1450_g_at	down	0.083974175	proteasome (prosome, macropain) subunit, alpha type, 4
34469_at	up	0.084001125	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
39010_at	down	0.084111642	endosulfine alpha
38409_at	down	0.084142918	sperm specific antigen 2
33237_at	down	0.084175575	RNA helicase
31502_at	up	0.084292511	annexin A2
559_s_at	up	0.084353486	T-cell leukemia, homeobox 1
34760_at	down	0.08437959	C-type lectin BIMLEC precursor
1464_at	up	0.084410452	
38295_at	down	0.084421315	pre-B-cell leukemia transcription factor 2
40318_at	up	0.084546986	dynein, cytoplasmic, intermediate polypeptide 1
38350_f_at	down	0.084601034	tubulin, alpha 2
41870_at	up	0.084650654	lung type-I cell membrane-associated glycoprotein
32058_at	up	0.084659847	carbohydrate sulfotransferase 10
36994_at	up	0.084686096	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
38681_at	down	0.084759916	eukaryotic translation initiation factor 3, subunit 6 48kDa
1069_at	down	0.08476962	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
40407_at	down	0.084769798	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
36986_at	up	0.084799441	lysophospholipase II
36102_at	down	0.084832731	voltage-dependent anion channel 3
38972_at	down	0.08489681	hypothetical protein BC013764
1854_at	up	0.084942696	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
32152_at	up	0.084966808	ankyrin 1, erythrocytic
31968_at	up	0.084975489	



39673_i_at	up	0.084986743	extracellular matrix protein 2, female organ and adipocyte specific
1441_s_at	down	0.085018907	tumor necrosis factor receptor superfamily, member 6
38619_at	up	0.085083592	golgi SNAP receptor complex member 2
37138_at	up	0.085132288	KIAA0809 protein
39793_at	down	0.085149958	glioblastoma amplified sequence
1060_g_at	up	0.085200706	neurotrophic tyrosine kinase, receptor, type 3
36647_at	down	0.085228019	hypothetical protein FLJ10326
40155_at	down	0.085237267	actin binding LIM protein 1
36538_at	up	0.085374834	protein phosphatase 1, regulatory (inhibitor) subunit 13B
41405_at	up	0.08539692	secreted frizzled-related protein 4
33842_at	up	0.085425991	hypothetical protein FLJ11560
644_at	up	0.085440532	ras homolog gene family, member N
1615_at	up	0.085579584	BCL2-like 1
40102_at	down	0.08561703	oxysterol binding protein-like 2
40824_at	down	0.085638027	exportin 7
37820_at	up	0.085679373	proline dehydrogenase (oxidase) 2
36310_at	up	0.085731979	keratin, hair, acidic, 1
1935_at	up	0.085805182	Mdm4, transformed 3T3 cell double minute 4, p53 binding protein (mouse)
40218_at	up	0.085816577	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1
33201_at	up	0.085854381	lethal giant larvae homolog 1 (Drosophila)
34439_at	up	0.085866067	absent in melanoma 2
40210_at	down	0.086009164	RAB13, member RAS oncogene family
41768_at	down	0.086063925	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
33089_s_at	down	0.08610984	ephrin-A2
33914_r_at	up	0.086112896	ferrochelatase (protoporphyrin)
35512_at	up	0.086129344	
37951_at	up	0.086142772	deleted in liver cancer 1
40033_at	up	0.086265844	mitogen-activated protein kinase 11
40801_at	down	0.08636791	DKFZP434C212 protein
41662_at	down	0.086379918	DKFZP566B183 protein
40437_at	down	0.086444658	DKFZP564G2022 protein
34326_at	down	0.08654165	coatamer protein complex, subunit beta
38924_s_at	down	0.086590576	spectrin SH3 domain binding protein 1
39721_at	up	0.086598108	ephrin-B1
36283_at	up	0.086609599	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase 54kDa)

41125_r_at	up	0.086618972	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)
38985_at	down	0.086620716	leptin receptor overlapping transcript-like 1
33705_at	down	0.086752173	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 duncce homolog, Drosophila)
33378_at	down	0.086759624	IDN3 protein
37706_at	up	0.086771534	golgi apparatus protein 1
40126_at	up	0.086915064	paired mesoderm homeo box 1
38040_at	down	0.086916527	splicing factor 30, survival of motor neuron-related
1711_at	up	0.086923062	tumor protein p53 binding protein, 1
1317_at	up	0.086948161	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
38403_at	down	0.086971119	lysosomal-associated membrane protein 2
33657_at	down	0.086989849	ribosomal protein L34
36537_at	down	0.087068338	Rho-specific guanine nucleotide exchange factor p114
37027_at	down	0.087167604	AHNAK nucleoprotein (desmoyokin)
1149_at	down	0.087172748	
34725_at	up	0.087190996	glucocorticoid receptor DNA binding factor 1
38035_at	down	0.087230646	myotubularin related protein 6
1489_s_at	up	0.087275505	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)
340_at	up	0.087320254	matrilin 3
521_at	up	0.087361038	metallothionein IV
39717_g_at	down	0.087391993	mitochondrial ribosomal protein L33
40633_at	up	0.087439293	mitotic control protein dis3 homolog
36165_at	down	0.087457854	cytochrome c oxidase subunit VIc
31735_at	up	0.087477585	type 1 protein phosphatase inhibitor
31417_at	up	0.087483514	hypocretin (orexin) neuropeptide precursor
38062_at	up	0.087507618	guanine nucleotide exchange factor for Rap1
38106_at	down	0.087527635	TGF beta-inducible nuclear protein 1
34272_at	up	0.087592461	regulator of G-protein signalling 4
34225_at	up	0.087596552	Wolf-Hirschhorn syndrome candidate 2
41712_at	down	0.087689972	likely ortholog of mouse aquarius
378_s_at	up	0.087796914	GPI anchored molecule like protein
31981_at	up	0.087831344	crystallin, beta B3
899_at	up	0.087862483	Indian hedgehog homolog (Drosophila)
40933_f_at	up	0.087878586	zinc finger, DHHC domain containing 18
32590_at	down	0.087886008	nucleolin

1397_at	down	0.088027982	mitogen-activated protein kinase kinase kinase 11
38821_at	down	0.088036116	progesterone receptor membrane component 2
41185_f_at	down	0.088044825	SMT3 suppressor of mlf two 3 homolog 2 (yeast)
40384_at	up	0.088045667	nephronophthisis 1 (juvenile)
39019_at	down	0.088056769	lysosomal-associated protein transmembrane 4 alpha
676_g_at	up	0.088222263	interferon induced transmembrane protein 1 (9-27)
41389_s_at	up	0.088364655	renal tumor antigen
239_at	down	0.08844228	cathepsin D (lysosomal aspartyl protease)
1842_at	down	0.088450446	
34134_at	up	0.088462035	
36885_at	down	0.08846417	spleen tyrosine kinase
39489_g_at	up	0.088500732	protocadherin 9
35857_at	up	0.088519565	glutamate receptor, ionotropic, kainate 1
37639_at	up	0.088520319	hepsin (transmembrane protease, serine 1)
AFFX- HUMTFRR/M11507 _5_at	up	0.088539866	transferrin receptor (p90, CD71)
35367_at	down	0.088573711	lectin, galactoside-binding, soluble, 3 (galectin 3)
35957_at	down	0.088641618	stannin
31458_at	up	0.088655659	cytokeratin 2
33192_g_at	down	0.08877997	chromosome 10 open reading frame 6
36523_at	down	0.0887804	ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)
32658_at	up	0.08879375	SAC2 suppressor of actin mutations 2-like (yeast)
36547_r_at	up	0.088847765	KIAA0542 gene product
32866_at	up	0.08900188	KIAA0605 gene product
36336_s_at	up	0.089108577	KIAA0963 protein
38031_at	down	0.089210079	KIAA0111 gene product
32771_at	up	0.089236711	group-specific component (vitamin D binding protein)
33368_at	down	0.089256532	protease, serine, 15
34441_at	up	0.089294655	
38258_at	up	0.089315852	
34143_at	up	0.089329234	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)
39199_at	up	0.08937154	

37034_at	down	0.089374662	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
578_at	up	0.089382491	recombination activating gene 2
35866_at	down	0.089442342	zinc finger protein 268
551_at	down	0.089610262	E1A binding protein p300
32003_at	up	0.089725235	methionine adenosyltransferase I, alpha
1541_f_at	up	0.089862891	interferon, alpha 6
39466_s_at	up	0.089866338	
324_f_at	down	0.089873012	
41310_f_at	up	0.089892054	nuclear receptor subfamily 2, group F, member 6
41808_at	down	0.090154156	cyclin D binding myb-like transcription factor 1
33037_at	up	0.090155577	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7
31466_at	up	0.090205249	major histocompatibility complex, class II, DR beta 6 (pseudogene)
37323_r_at	up	0.090262072	hydroxyprostaglandin dehydrogenase 15-(NAD)
2091_at	up	0.090282876	wingless-type MMTV Integration site family, member 4
32477_at	up	0.090315491	calpain 9 (nCL-4)
34832_s_at	up	0.090482967	KIAA0763 gene product
AFFX-PheX-5_at	up	0.090493351	
39141_at	up	0.090696236	ATP-binding cassette, sub-family F (GCN20), member 1
38402_at	down	0.090789867	lysosomal-associated membrane protein 2
34109_at	up	0.090803494	proline dehydrogenase (oxidase) 1
40440_at	up	0.090928291	PAI-1 mRNA-binding protein
34387_at	down	0.091050579	KIAA0205 gene product
40639_at	up	0.09105652	SCO cytochrome oxidase deficient homolog 2 (yeast)
33289_f_at	down	0.091058	zinc finger protein 263
41476_at	up	0.091067637	
35661_g_at	up	0.091173127	S-antigen; retina and pineal gland (arrestin)
39959_at	up	0.091197187	ubiquitin D
35129_at	up	0.091246944	sperm adhesion molecule 1 (PH-20 hyaluronidase, zona pellucida binding)
1879_at	down	0.091260491	related RAS viral (r-ras) oncogene homolog
37734_at	down	0.091272658	disco-interacting protein 2 (Drosophila) homolog
39680_at	up	0.09128097	statherin

1300_at	up	0.091302081	X-ray repair complementing defective repair in Chinese hamster cells 2
35494_at	up	0.091514972	
AFFX-DapX-3_at	up	0.091526914	
35159_at	up	0.091541071	tubulin-specific chaperone e
1686_g_at	down	0.091586384	S-phase response (cyclin-related)
38243_at	up	0.091608235	neural cell adhesion molecule 1
41772_at	up	0.091636193	monoamine oxidase A
36468_at	up	0.091669779	dystrobrevin, alpha
31912_at	up	0.091687981	forkhead box H1
1966_i_at	up	0.091745212	nitric oxide synthase 2C
32392_s_at	up	0.091772778	UDP glycosyltransferase 1 family, polypeptide A4
40854_at	down	0.091958912	ubiquinol-cytochrome c reductase core protein II
37326_at	down	0.091968595	proteolipid protein 2 (colonic epithelium-enriched)
33835_at	up	0.092020494	KIAA0721 protein
32666_at	up	0.092098111	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
34101_at	up	0.092129007	
33792_at	up	0.092178872	prostate stem cell antigen
38008_at	up	0.092208168	DNA segment on chromosome 4 (unique) 234 expressed sequence
33103_s_at	down	0.092213362	adducin 3 (gamma)
1448_at	down	0.092287738	proteasome (prosome, macropain) subunit, alpha type, 3
36213_at	up	0.092306281	malignant fibrous histiocytoma amplified sequence 1
37677_at	down	0.092335261	phosphoglycerate kinase 1
40374_at	up	0.092357025	cardiac ankyrin repeat protein
34264_at	up	0.092400894	RUN and SH3 domain containing 1
36925_at	up	0.092424153	heat shock 70kDa protein 2
39003_at	down	0.092431788	pituitary tumor-transforming 1 interacting protein
41795_at	down	0.09245412	NCK adaptor protein 1
31906_at	down	0.092499322	heat shock factor binding protein 1
34188_at	down	0.092551592	
38019_at	up	0.092684992	casein kinase 1, epsilon
38673_s_at	down	0.092735744	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
34814_at	down	0.092753688	SUMO-1 activating enzyme subunit 2
38212_at	up	0.092799885	UDP-N-acetyl-alpha-D-galactosamine:(N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase (GalNAc-T)
31379_at	up	0.092814218	HFSE-1 protein

34578_at	up	0.092823397	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)
41545_at	up	0.092876791	cyclin-dependent kinase 6
38037_at	up	0.092905054	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)
41788_i_at	down	0.092989382	KIAA0669 gene product
32624_at	down	0.093011872	likely ortholog of mouse tuberin-like protein 1
34122_at	up	0.093042118	casein beta
36553_at	down	0.093052406	acetylserotonin O-methyltransferase-like
32679_at	up	0.093083461	likely ortholog of chicken chondrocyte protein with a poly-proline region
37117_at	up	0.093191269	Rho GTPase activating protein 8
36077_at	down	0.093212186	RAB, member of RAS oncogene family-like 4
38854_at	up	0.093242092	KIAA0635 gene product
34118_at	up	0.093250389	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 2 polypeptide
36414_s_at	down	0.093282245	calcium/calmodulin-dependent serine protein kinase (MAGUK family)
32094_at	up	0.093290429	carbohydrate (chondroitin 6) sulfotransferase 3
41137_at	up	0.093310928	protein phosphatase 1, regulatory (inhibitor) subunit 12B
41149_at	up	0.093394734	exonuclease NEF-sp
35268_at	down	0.093406671	axotrophin
33352_at	down	0.093411658	histone 2, H2be
31463_s_at	down	0.093412524	
38190_r_at	up	0.093548584	KIAA0645 gene product
40864_at	down	0.093610502	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
40903_at	down	0.093640616	ATPase, H <sup>+</sup> transporting, lysosomal interacting protein 2
31874_at	down	0.093647357	growth arrest-specific 2 like 1
33820_g_at	down	0.093671525	lactate dehydrogenase B
35311_at	down	0.093773374	cellular repressor of E1A-stimulated genes
36350_at	up	0.093885805	
39663_at	down	0.093917507	mannosidase, alpha, class 2A, member 1
35149_at	up	0.093949795	tumor necrosis factor receptor superfamily, member 5
38451_at	down	0.093966652	ubiquinol-cytochrome c reductase (6.4kD) subunit

31330_at	down	0.093994243	ribosomal protein S19
34329_at	down	0.094055721	p21 (CDKN1A)-activated kinase 2
40919_at	up	0.094079635	somatostatin receptor 2
41215_s_at	down	0.094096263	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
31901_at	up	0.094118872	potassium voltage-gated channel, shaker-related subfamily, beta member 2
1081_at	down	0.094220232	ornithine decarboxylase 1
41194_at	down	0.094258686	signal recognition particle 14kDa (homologous Alu RNA binding protein)
37098_at	up	0.09434038	protoporphyrinogen oxidase
39056_at	down	0.094461372	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
37527_at	up	0.094565974	ELK3, ETS-domain protein (SRF accessory protein 2)
35998_at	up	0.094588743	
35328_at	up	0.094596866	
31815_r_at	up	0.094601451	low density lipoprotein receptor-related protein 3
34282_at	down	0.094675793	nuclear factor (erythroid-derived 2)-like 3
36463_at	down	0.094675835	BCL2-associated athanogene 5
37679_at	down	0.094863772	interferon-related developmental regulator 1
34062_at	up	0.094905599	ets variant gene 2
40080_at	up	0.094934258	KIAA0090 protein
41414_at	up	0.094942383	chromosome 22 open reading frame 3
40977_f_at	up	0.095014531	cerebellar degeneration-related protein 1, 34kDa
35897_r_at	up	0.095044456	brain-specific angiogenesis inhibitor 1
1428_at	down	0.095078801	
37773_at	up	0.095087394	KIAA1005 protein
40431_at	down	0.095109067	KIAA0431 protein
36203_at	down	0.095163871	ornithine decarboxylase 1
444_g_at	up	0.095292483	homeo box D4
1244_at	up	0.095328326	signal transducer and activator of transcription 2, 113kDa
39995_s_at	up	0.095391047	WW domain containing oxidoreductase
39178_at	down	0.095462475	reticulon 1
31706_at	up	0.09547677	
40023_at	up	0.095557348	brain-derived neurotrophic factor
34472_at	up	0.095594647	frizzled homolog 6 (Drosophila)
38950_r_at	up	0.095606306	matrix metalloproteinase 23B

1852_at	up	0.095612496	tumor necrosis factor (TNF superfamily, member 2)
41174_at	up	0.095643232	RAN binding protein 2-like 1
34761_r_at	down	0.095664289	a disintegrin and metalloproteinase domain 9 (meltrin gamma)
40449_at	up	0.095715432	replication factor C (activator 1) 1, 145kDa
35826_at	up	0.095727306	suppressor of Ty 5 homolog (S. cerevisiae)
700_s_at	up	0.09583438	
582_g_at	down	0.095875255	nuclear receptor subfamily 2, group C, member 1
39244_at	down	0.095915812	RAB4A, member RAS oncogene family
32899_s_at	up	0.095919044	RAR-related orphan receptor A
32296_at	up	0.095927535	carbonic anhydrase VA, mitochondrial
36679_at	down	0.095972007	signal recognition particle receptor ('docking protein')
31885_at	up	0.095999682	protein tyrosine phosphatase, non-receptor type 3
368_at	up	0.096090928	trophoblast glycoprotein
36313_at	down	0.096111046	ecotropic viral integration site 2A
41367_at	up	0.09615194	hepatocyte nuclear factor 4, gamma
34610_at	down	0.096189258	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1
41093_at	up	0.096218086	opioid binding protein/cell adhesion molecule-like
38093_at	down	0.096246266	chromosome 14 open reading frame 32
35345_at	up	0.096248258	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)
40976_at	up	0.09628133	katanin p80 (WD repeat containing) subunit B 1
32295_at	up	0.096300607	HLA complex group 9
1636_g_at	up	0.096306453	v-abl Abelson murine leukemia viral oncogene homolog 1
35595_at	up	0.096330447	calcitonin gene-related peptide-receptor component protein
40533_at	up	0.096342646	baculoviral IAP repeat-containing 5 (survivin)
1261_i_at	up	0.096407666	glutathione S-transferase A2
32567_at	up	0.096421885	choline kinase
36100_at	up	0.096473819	vascular endothelial growth factor
40256_at	up	0.09651525	
37747_at	down	0.096606126	annexin A5
37764_at	up	0.096642303	holocarboxylase synthetase (biotin-[propionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] ligase)
34613_at	up	0.096690958	KIAA1086 protein



615_s_at	up	0.09674634	parathyroid hormone-like hormone
31827_s_at	up	0.096759998	trans-golgi network protein 2
32011_g_at	up	0.096816474	hypothetical protein EAN57
33086_at	up	0.096895282	prophet of Pit1, paired-like homeodomain transcription factor
34942_at	up	0.097018589	hypothetical protein FLJ38993
39578_at	up	0.097121586	hairless
41460_at	down	0.097154944	RNA binding motif protein 14
31713_s_at	up	0.097197158	discs, large (Drosophila) homolog-associated protein 2
32277_at	up	0.097229418	potassium voltage-gated channel, shaker-related subfamily, member 3
462_at	up	0.097234978	nuclear factor I/B
35187_at	down	0.097264305	
38033_at	up	0.097281795	DKFZP564M1416 protein
464_s_at	down	0.097305326	interferon-induced protein 35
41120_at	up	0.097408034	aminomethyltransferase (glycine cleavage system protein T)
40381_at	up	0.097503532	KIAA0972 protein
41587_g_at	up	0.097533335	fibroblast growth factor 18
39825_at	up	0.097585237	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1
1822_at	up	0.097654682	
32178_r_at	down	0.097713503	synaptosomal-associated protein, 23kDa
1447_at	down	0.097772909	proteasome (prosome, macropain) subunit, beta type, 1
33930_at	down	0.097850141	chromosome 14 open reading frame 163
36353_at	up	0.097867455	hairy and enhancer of split (Drosophila) homolog 2
35093_at	up	0.097907561	purinergic receptor P2X-like 1, orphan receptor
1357_at	down	0.09799221	ubiquitin specific protease 4 (proto-oncogene)
37280_at	up	0.098054947	MAD, mothers against decapentaplegic homolog 1 (Drosophila)
1907_at	up	0.098069395	retinoblastoma-like 1 (p107)
33141_at	up	0.098156986	hydroxysteroid (17-beta) dehydrogenase 1
39686_g_at	down	0.098160911	like mouse brain protein E46
37673_at	down	0.09818696	neutral sphingomyelinase (N-SMase) activation associated factor
38110_at	down	0.098232139	syndecan binding protein (syntenin)
34879_at	down	0.098241379	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit

38609_at	up	0.098269966	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
37492_at	up	0.098274979	KIAA0500 protein
34100_at	up	0.098277118	
37996_s_at	up	0.098280565	dystrophia myotonica-protein kinase
35824_at	down	0.098305072	zinc finger protein 238
40086_at	down	0.098345702	friend of EBNA2
32083_at	down	0.098363125	transmembrane 7 superfamily member 1 (upregulated in kidney)
34977_at	down	0.09838151	sialic acid binding Ig-like lectin 7
33161_at	down	0.098418566	hypothetical protein MGC15523
37861_at	up	0.098434036	CD1E antigen, e polypeptide
38784_g_at	up	0.098470912	mucin 1, transmembrane
38020_at	down	0.098546526	KIAA0652 gene product
808_at	up	0.098588848	RAB27B, member RAS oncogene family
1695_at	down	0.098764335	neural precursor cell expressed, developmentally down-regulated 8
36130_f_at	up	0.098794417	metallothionein 1E (functional)
31612_at	up	0.098800032	secretoglobulin, family 1D, member 1
37900_at	down	0.099027962	peroxisomal biogenesis factor 11B
33809_at	up	0.099045406	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1
38722_at	up	0.099099373	collagen, type VI, alpha 1
36522_at	up	0.099155422	mucoepidermoid carcinoma translocated 1
2051_at	up	0.099167839	O-6-methylguanine-DNA methyltransferase
38907_at	up	0.099379332	
40860_s_at	up	0.099381562	nuclear protein UKp68
40880_r_at	up	0.099383953	chloride channel 3
41370_at	down	0.099417017	U5 snRNP-specific 40 kDa protein (hPrp8-binding)
36968_s_at	down	0.099572253	Opa-interacting protein 2
32325_at	up	0.099581291	
33524_at	up	0.099592485	v-crk sarcoma virus CT10 oncogene homolog (avian)-like
33388_at	up	0.099596344	testis expressed gene 261
35321_at	down	0.099608404	tousled-like kinase 2
36946_at	down	0.099667092	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
1348_s_at	down	0.099835885	propionyl Coenzyme A carboxylase, alpha polypeptide
41737_at	down	0.099885912	serine/arginine repetitive matrix 1

39558_s_at	up	0.099902424	
39474_s_at	up	0.099944447	cysteine knot superfamily 1, BMP antagonist 1
38825_at	up	0.099970407	fibrinogen, A alpha polypeptide
38164_at	down	0.099971672	retinitis pigmentosa GTPase regulator

### EXAMPLE 3: PROSTATE TUMOR DIAGNOSIS THROUGH BLOODCELL MULTIGENE SIGNATURES

#### Introduction

5 Prostate cancer is the second largest cancer killer of men in the United States and Europe. It has been estimated that in 2000, in the U.S., 180,400 men were diagnosed with prostate cancer and approximately 32,000 died in that year alone (Greenlee *et al.*, CA Cancer J Clin. 2000; 50(1):7-33). Current techniques for the screening and risk assessment of prostate cancer, as a prerequisite to surgical biopsy procedures, are based upon the  
10 measurement of either individual serum biomarkers, or expression of individual genes in circulating malignant cells (Oesterling *et al.*, JAMA 1993; 270(7):860-4; Seaman *et al.*, Urol Clin North Am.; 1993; 20(4):653-63; and Catalona *et al.*, Urology 2000; 56(2):255). These techniques, which include RT-PCR, possess a number of limitations, including lack of specificity and accuracy in the diagnosis and, also a lack of prognostic information. This  
15 ultimately yields high numbers of false positive diagnoses, and consequently unnecessarily large numbers of surgical biopsies.

Since its clinical approval by the FDA in 1986, prostate specific antigen (PSA) has been recognized as the most useful biomarker for diagnosis and surveillance of prostate cancer. In current clinical practice, a serum PSA assay (which quantifies levels of PSA  
20 protein as ng/ml in sera prepared from peripheral blood), in conjunction with digital rectal examination (DRE), is used to indicate which patients should undergo prostate biopsy. Prostate cancer statistics have clearly shown that pre-screening prior to biopsy has led to both an increase in the number of men diagnosed with cancer and a decline in age of diagnosis due to earlier detection (Roberts *et al.*, Urology. 2000;56(5):817-22). It was  
25 estimated that during 1997, over 750,000 prostate biopsies were performed following PSA and DRE screening (ref). However, although for example PSA is an effective indicator of prostate cancer when serum levels are high, diagnostic assays based on this marker become

more ambiguous when levels are only moderately elevated, i.e.i.e. between 2-10 ng/ml. Abnormal findings from DRE have also been attributed to various benign conditions, thus contributing to this low accuracy of cancer detection rates prior to biopsy (Roberts *et al.*, Urology. 2000;56(5):817-22). A false-positive pre-biopsy diagnosis of cancer has been  
5 reported in 40-66% of men with both abnormal DRE and PSA levels greater than 4ng/ml, resulting in a high percent of unnecessary prostate biopsies (Bangma *et al.*, J Urol. 1997;157(6):2191-6; Smith *et al.*, Cancer. 1997;80(9):1852-6; Roberts *et al.*, Urology. 2000;56(5):817-22).

Although methods have been investigated to increase specificity of PSA, such as the  
10 use of free/total PSA measurements (Catalona *et al.*, Urology 2000; 56(2):255), a recent review of screening programs has suggested that even though the use of free/total PSA serum measurements may reduce the need for biopsy by up to 40%, approximately 12% of all tumors would still be missed with this assay (Neal *et al.*, Eur J Cancer 2000; 36(10):1316-21). In addition, serum quantitation of biomarkers, such as PSA, does not  
15 reliably correlate with important cancer variables such as biological aggressiveness, does not allow outcome predictions in patients with hormone refractory disease (Murphy *et al.*, Cancer. 1998;83(11):2259-69), and does not identify the presence of soft tissue metastasis (Beckett *et al.*, Clin Cancer Res. 1999;5(12):4034-40). For example, in over  
20 half of patients with metastatic disease, diagnosis was made only after radical surgery for the localized tumor (Olsson CA. Urol Clin North Am. 1997;24(2):367-78). Current research has implied that important diagnostic and prognostic information will be derived only after surgical procedures, where biopsy or radical prostatectomy specimens are surgically removed, and tumor pathology is classified by histological grade and Gleason score. Unfortunately, these invasive methods also have some limitations, such as the need for a  
25 highly trained pathologist to interpret the degree of tumor pathology and the histological grade of clinical specimens and the requirement for repeat biopsies in some patients because of missed tumors (Lee *et al.*, Prostate 1999;39(3):213-8; Noguchi *et al.* Int J Urol 1999;6:7-12), and one study reported that up to 26% of men with an initial non-cancer diagnosis were reported positive for prostate cancer on a repeated biopsy performed within  
30 one year (O'Dowd *et al.*, Urology. 2000;55(4):553-9). Patient discomfort and stress is also very high in diagnostic tests based on surgical tissue removal.

There is growing evidence that individuals with prostate cancer and other forms of malignant disease exhibit immune responses that can be detected at the level of altered gene expression in leukocytes circulating in peripheral blood. Furthermore, the use of microarray technology allows the simultaneous measurement of the expression levels of up to 14,000 genes transcribed in circulating leukocytes derived from the blood of prostate cancer patients and control individuals. This technology described in this invention demonstrates that individuals suffering from prostate cancer exhibit a conserved pattern, or signature, of gene expression levels in their peripheral blood leukocytes, which is distinct from the corresponding pattern of expression in leukocytes from control subjects. In addition, patients with prostate tumors at different histological grades may yield distinct expression signatures that reflect the biological stage and aggressiveness of the tumor, and that information can thus be employed to differentiate among tumors at different pathological stages.

This Example demonstrates a novel technique that does not require invasive surgery, yet provides an accurate diagnosis of prostate cancer, and may also provides detailed prognostic information on the stage and biological aggressiveness of the tumor. Investigators have begun to employ microarray technology, based upon sample cDNA probe hybridization to DNA microarrays, to identify and isolate genes differentially expressed in prostate tumor tissues and prostate cancer cell lines. Recent studies have identified genes that may be involved in hormone refractory prostate cancer (Amler *et al.*, Cancer Res. 2000; 60(21):6134-41), and genes that are potential targets for prostate cancer therapy. Many others have applied microarray technology to investigate the LNCaP tumor model cell line series, which re-capitulates some of the major biological stages of prostate tumor progression. These studies have identified genes thought to play a role in the progression of prostate cancer from androgen -and bone cell- growth dependence to autonomous metastatic ability (Clelland *et al.*, Am.J.Hum.Genet. 2000; 67:(4) 8).

An alternative approach to these experiments has been the development of prostate tissue microarrays, where sectioned tumor tissue is arrayed and immobilized onto the microarray surfaces. Tissue arrays allow more detailed analysis of gene expression within individual prostate tumor cells and has been used to determine and compare profiles of gene expression between tissues of men from ethnic populations that have both low and high risk

for developing cancer. Cole *et al.* (Nat Genet. 1999: 21(1 Suppl):38-41) have proposed the use of tissue microarrays to determine a combined, detailed histological and gene expression 3D reconstruction of the anatomy of normal and prostate malignant tissues, which may ultimately provide vital information in the cellular progression of the disease.

5 Two new studies have been published that are likely to be of great clinical significance for the management of prostate cancer. In one investigation, published in *Nature*, Dhanasekaran *et al.*, employed normal and neoplastic prostate specimens and cDNA microarrays to analyze and identify gene expression patterns of normal and tumor tissue (Dhanasekaran *et al.*, *infra*). This study was the first to report specific expression  
10 signatures that could distinguish prostate tissue, including normal prostate (adjacent to the tumor site), BPH, localized prostate cancer and metastatic, hormone refractory disease. More recently, a group has employed Affymetrix GeneChip microarrays to analyze prostate tumor specimens and compare gene expression levels among samples of known stages of prostate cancer (Luo *et al.*, Mol Carcinog 2002;33(1):25-35.). Cluster analysis of the  
15 measured expression levels identified gene-specific expression patterns from highly aggressive prostate tumors that were distinct from patterns of gene expression in organ confined disease tissue (Luo *et al.*, *supra*).

However, although these investigations of solid tumors provide detailed information on the pathology and malignant process of the tumor, invasive surgery is always necessary  
20 to obtain the tumor tissue studied. In contrast, this Example investigates the feasibility of a microarray-based diagnostic test that measures the levels of RNA transcribed from peripheral blood leukocytes of each individual at risk for prostate cancer, and thus does not require surgery to obtain each diagnostic sample.

Studies have shown that cancer patients exhibit immune responses that differ from  
25 those of control individuals. These studies have also demonstrated that this response can be detected at the level of altered expression of individual genes, e.g., cytokine genes, in leukocytes within peripheral blood. This example employs microarray technology to quantify the gene expression levels of thousands of genes in each prostate cancer patient and control subject's blood sample, permitting the determination of leukocyte gene  
30 expression patterns, or signatures, for each prostate cancer patient and control subject

analyzed. Pattern analysis algorithms compare these expression signatures, and define patterns that can distinguish both between normal individuals and those with cancer, and also between patients with prostate tumors at different stages of biological progression. Identification of a leukocyte multigene expression signature specific to prostate cancer, and  
5 also characteristic for pathologically defined stages of prostate cancer, provides both diagnostic and prognostic information on individual tumors, and thus play a vital role in prostate cancer pre-biopsy population screens.

The results from this experiment form the basis of a pre-biopsy diagnostic screen.

A clinical assay initially involves the hybridization of a labeled probe synthesized from  
10 RNA extracted from a blood sample drawn from the individual at risk for prostate cancer to a microarray containing a number of genes that are differentially expressed between cancer patients and control individuals. The resultant expression pattern is then compared to a set of known multigene signatures, specific for individual stages of tumor progression for a non-invasive prostate cancer diagnostic assay that can yield both diagnostic and staging  
15 information for each individual at risk.

Furthermore, since this assay will measure gene expression within leukocytes, instead of circulating malignant cells, and does not rely on the measurement of biomolecules secreted from malignant cells, the resultant assay is sensitive and accurate, and capable of detecting tumors that are still at an early stage of malignancy. Such an  
20 assay serves as an important pre-screen that can, with a minimum of patient discomfort, identify men with prostate cancer.

Data from investigations of ratios of T cell subsets provides some evidence to correlate serum cytokine levels with mRNA levels (detected by RT-PCR), within peripheral blood from cancer patients. It is therefore likely that the differential prognostic serum  
25 levels measured from prostate cancer patient blood will also be detected at the level of mRNA expression. The experimental procedure follows the expression levels of each of the genes mentioned above, and thus determine whether previously reported increases or decreases in serum protein levels in cancer patients correlate with the corresponding mRNA levels detected by microarray analysis.

In the work described by Veltri *et al.*, Strom *et al.*, *supra* and in the other investigations described above, mRNA levels have been quantified individually by RT-PCR techniques. However, this would be extremely time-consuming if many genes were to be analyzed in one experiment. In contrast, this Example employs microarray technology to quantify mRNA transcripts, which allows the simultaneous analysis of thousands of genes expressed in peripheral blood leukocytes. The complex differential gene expression measured using this approach identifies patterns or signatures of gene expression that differ between prostate cancer patients and control subjects, and thus forms the basis of a diagnostic technique.

It seems clear that the use of multiple gene products for the determination of expression signatures provides considerably more detailed information on tumor stage and prognosis than can be provided by the quantitation of individual serum protein levels.

It should also be noted that although leukocyte gene expression levels will be measured, if, *e.g.*, malignant prostate cells were also present in the blood of patients, then gene expression of these cells will also be quantified. However, it seems likely that the detection of gene expression of malignant cells within blood would actually increase the specificity of this analysis, as mRNA levels arising from circulating metastatic cells would differ from mRNA levels in patients with no metastatic cells in their blood stream.

### Microarray Technology

**Oligonucleotide Microarrays.** There are two major types of microarray technology; spotted cDNA arrays and manufactured oligonucleotide arrays. The present invention employs high density oligonucleotide Affymetrix® GeneChip arrays (reviewed in Schena *et al.*, Trends Biotechnol. 1999; 16(7):301-6). The Affymetrix system was chosen due to: 1) the large numbers of gene sequences represented within the array, 2) the highly developed Affymetrix protocols for probe preparation and microarray hybridization, and 3) the built-in multiple internal standards. In addition, custom designed normalization software for accurate comparison of results between each individual hybridization accommodates the experimental plan, which involves a direct comparison between individual microarray experiments.



A recent investigation of the reproducibility of DNA microarrays has highlighted some problems of reproducibility and comparison among array hybridizations, and the need for replicate experiments. Use of the Affymetrix system eliminates some of the problems that are associated with other microarray technologies, because it provides a significantly  
5 lower variation between experiments.

***Pattern Analysis Algorithms and Computer Analysis.*** After scanning of each microarray to detect the hybridization signals, Affymetrix® Microarray Suite software is employed for image acquisition and normalization of the fluorescent signals using internal standards. Analysis of the resultant signal intensities over each oligonucleotide, or data  
10 point, within each experiment then falls into two main categories: Supervised Learning Algorithms (Golub *et al.*, *infra*; Slonim *et al.*, 1999; Yeang *et al.*, Bioinformatics. 2001;17 Suppl 1:S316-22; Ramaswamy *et al.*, *infra*); and Hierarchical Clustering (Eisen *et al.*, *infra*; Alizadeh *et al.*, *infra*; Perou *et al.*, Nature 2000; 406(6797):747-52). All algorithms employed have the capacity to analyze the very large data-sets, and allow comparisons of  
15 multiple experiments and multiple points within a single experiment.

Affymetrix oligonucleotide microarray technology is employed to simultaneously measure the expression levels of up to about 14,000 genes transcribed in circulating leukocytes derived from the peripheral blood of 40 prostate cancer patients and 20 control individuals. Briefly, leukocytes are extracted from whole blood obtained from prostate  
20 cancer patients and healthy controls, and the RNA isolated from these cells is employed to synthesize cDNA, which is then itself employed as a template to synthesize labeled cRNA for hybridization to Affymetrix microarrays. The expression patterns generated for each individual subject sample are compared using data analysis algorithms that have the ability to identify and record multigene expression levels as patterns or multigene signatures.

25 In a specific experiment, leukocytes are collected and subject to sample processing and microarray hybridization. Expression data is derived from microarray hybridization plus data-analysis algorithms to generate multigene expression patterns. The evidence shows that circulating blood leukocytes in individuals suffering from prostate cancer exhibit a characteristic signature of gene expression levels that is different from the signature  
30 exhibited by circulating leukocytes from control subjects. Multigene expression signatures

in individuals with prostate cancer are specific to the aggressiveness of the tumor from the individual examined, and thus reflect the stage the malignancy has reached in the patient.

### **Materials and Methods**

***Prostate Cancer Subjects.*** Prostate cancer patients are derived from those undergoing radical prostatectomy (n=50 per year), and those undergoing radiation seed implant therapy (n=150 per year). The total population of prostate cancer patients will be screened for possible recruitment into this study. Informed consent is obtained, according to Institutional Board Regulations. Blood drawing takes place prior to radical surgery or seed implantation.

Each patient recruited to participate in this study is provided with a questionnaire designed to obtain both demographic information and information on current general health. The questionnaire is approved by the Institutional Review Board. Clinical information and pathology reports is also collected for this study. This documentation includes patient history of serum PSA tests, all results of prostatic needle biopsy (Gleason's stage) and/or clinical and pathological analysis of tumor tissue following surgery (TNM scale, pT stage). CBCs are performed on all recruited patients following blood drawing. Each patient record also has dates of any previous needle biopsy, or other surgical procedures (on average 3-6 months prior to the biopsy).

***Exclusion Criteria.*** Patients are excluded if: 1) they have had surgery or other physical trauma less than six weeks prior to blood collection, 2) if they have abnormal CBCs, 3) if they have a current infection, 4) if they have autoimmune disease, 5) if they have had chronic use of immunosuppressants or anti-inflammatory medication. These exclusion criteria have been designed to reduce the likelihood of including prostate cancer patients that exhibit leukocyte gene expression that is different from healthy control subjects, but that arises from factors other than growth and development of a prostate tumor, such as an immune response to surgery or the presence of an infectious agent.

Expression signature assays include the screening, recruitment, blood drawing and leukocyte sample preparation of prostate cancer patients. Following removal of red blood cells, the leukocyte cell samples are stable at -70° C for long periods of time. For each subject, blood will be drawn, processed to isolate leukocyte cells, and then stored at -70° C.

Subjects are chosen for complete processing (which involves the extraction of RNA, synthesis of cDNA and cRNA, and microarray hybridization) based on the criteria described below.

Microarray analysis measures gene expression levels from 40 of the leukocyte samples collected. The expression data are subjected to supervised learning and clustering algorithms to identify and determine leukocyte gene expression patterns that distinguish between prostate cancer patients and healthy controls.

The expression data generated are then used to distinguish among leukocyte gene expression patterns of prostate cancer patients at different diagnosed stages of tumor progression. All patients undergoing treatment, and who are recruited into this study, will have documented reports following needle biopsy (a Gleason score can be documented for each subject). For those patients undergoing radiation seed implantation, further pathological information are not available. Tumors of prostate cancer patients with clinically localized disease can be staged after prostatectomy by the TNM scale (T1, T2 and T3), and also given a more accurate pT stage. The expression data only of men with pathological staging, and thus only of those who will undergo radical surgery are evaluated. Assuming a conservative 20% recruitment of all radical prostatectomy patients (which is below current recruitment levels of prostate cancer subjects), greater than 20 subjects are recruited over the two year period of this proposal.

This experiment involves recruitment of subjects, extraction of leukocytes and completed sample processing for every prostate cancer patient who satisfies the following criteria: undergoes radical prostatectomy or radiation seed implantation, consents to take part in this proposal, does not fall within the exclusion criteria, and has detailed tumor stage information available.

**Control Subjects.** Twenty control male subjects, approximately age-matched to prostate cancer patients, are recruited from the staff and staff relatives. Informed consent is obtained, according to Institutional Board Regulations. Each control subject recruited to participate in this study is provided with a questionnaire to obtain both demographic information and information on current general health. The questionnaire is approved by the Institutional Review Board. Information collected through the completion of this

questionnaire is employed as described above, as well as to determine that a control subject is unlikely to have an undiagnosed prostate tumor, or other solid tumor, that may effect leukocyte gene expression. Blood samples are drawn by a trained phlebotomist from the antecubital vein using a needle and evacuated tube. For each control subject chosen to take  
5 part in this study, serum PSA levels are measured, and CBC counts performed.

***Exclusion criteria for controls.*** Control subjects are excluded from this study if: 1) they have serum PSA levels  $>4\text{ng/ml}$ , 2) if they have abnormal CBCs, 3) if they have experienced discomfort while urinating, 4) if they have a first-degree relative diagnosed with prostate cancer or any other solid tumor, 5) if they have documented a current  
10 infection, 6) if they have autoimmune disease, 7) if they have had surgery or other physical trauma less than six weeks prior to blood collection, 8) if they have had chronic use of immunosuppressants or anti-inflammatory medication.

***Potential Problems Arising from Factors Other than Prostate Cancer.*** During recruitment of both prostate cancer patients and control subjects, it is clear that attention  
15 must be paid to the possibility that the mRNA levels of some of the genes expressed in leukocytes, in both patients and control subjects, may change because of underlying inflammatory disease states or other illness. As described above, both prostate cancer patients and control subjects are otherwise normal healthy individuals with no history of autoimmune disease or current infection. It is unlikely that any control subject has an  
20 undiagnosed prostate or other solid tumor.

However, it is well known that individuals possess different immune complements, and these may well be detected within individual experiments. Flagging is a method employed to normalize between patient samples and thus will be employed to reduce some of the inter-subject variability that may be detected following microarray hybridization.  
25 Any gene found to be significantly differentially expressed ( $>3$  fold change) between two or more of the normal control individuals, will be "flagged", which subsequently removes this gene from any further analysis. This method was successfully used to remove inter-subject variation from both multiple patient samples such as total lymph nodes, and also from multiple cell lines of different lineages that were employed to identify profiles of gene  
30 expression in B cell lymphomas (Alizadeh *et al.*, *supra*).

It should be noted that the algorithms described in detail below have been successfully employed to identify gene expression profiles that distinguish complex tumor tissue from normal non-disease tissue (that has not undergone micro-dissection procedures), and thus are not hindered by complex patterns of total gene expression.

5           ***Use of the Affymetrix Oligonucleotide Microarray Technology.*** The Affymetrix system appears to be better suited to the present project than a cDNA microarray-based system. Therefore, Affymetrix Human Genome U133A oligonucleotide microarrays are employed to analyze gene expression signatures in peripheral blood leukocytes taken from the prostate cancer patients described above, and in corresponding cells from control  
10 subjects recruited during this study. This array is an upgraded version of the HU95A arrays employed in the preliminary studies, and will soon replace this array. The arrays are comparable with each other.

Affymetrix Human U133A oligonucleotide microarrays contain about 14,000 individual human sequence verified oligonucleotides, representing Unigene, GenBank and  
15 TIGR database clusters that have been previously characterized by function and disease association. The specific gene products described above are all represented on this microarray and thus are included in all analytical procedures. Furthermore, many other genes known to be involved in immune responses are also included on this microarray, such as multiple cytokines and growth factors, *e.g.*, osteopontin, which has been found to be up-  
20 regulated in prostate tumor models (Thalmann *et al.*, Cancer Res. 1999; 54(10):2577-81), and shown functionally to play a role in cell mediated immunity.

***Sample Processing, Probe Preparation and Microarray Hybridization.*** All blood samples are processed immediately following collection; leukocytes are extracted from blood using lysis buffers and centrifugation, according to standard procedures. The  
25 leukocytes are stable at -70° C for long periods of time (> 6 months, Qiagen). The storage of leukocytes at that temperature allows the retrospective determination of which samples are to be hybridized to GeneChips, after a detailed analysis of all available patient history and a confirmed histological analysis of biopsy samples and prostate tissue in the case of patients undergoing surgery. All patient and control samples chosen for RNA extraction  
30 are processed in duplicate, by splitting the white blood cell sample extracted from whole

blood and processing the duplicate samples identically thereafter. The need for replicate microarray experiments has been previously highlighted, so each sample is processed in duplicate. This experimental design was based on the reproducibility of Affymetrix arrays, hybridization protocols and scanning (mean  $R^2=0.98$  and  $0.967$  for repeat hybridization, and duplicate sample processing respectively), and previously reported use of duplicate hybridizations in microarray experiments (Chen *et al.*, J Cell Biol 2000; 151:1321-36.).

**Data Analysis.** Following image acquisition and normalization using Affymetrix software and protocols, the data analysis employs two major algorithm types ; Hierarchical Clustering (Eisen *et al.*, *infra*; Alizadeh *et al.*, *infra*; Perou *et al.*, *infra*) and Supervised Learning Algorithms; Group Classification (Golub *et al.*, *supra*; Slonim *et al.*, *infra*), and Support Vector Machine (Yeang *et al.*, *supra*; Ramaswamy *et al.*, *infra*). Use of each of these techniques is described in detail below.

**Hierarchical Clustering.** Leukocyte expression signatures discriminate between cancer patients and control, matched subjects, and also to attempt to distinguish among individual stages of the prostate tumors analyzed. Data analysis initially employs a hierarchical clustering algorithm that has been successfully applied to classify gene expression data in several studies of human tumors, and is briefly described as follows. The Cluster program (M.Eisen), employs a fast two-way clustering that is based upon a similarity metric between genes and experimental samples. A standard Pearson correlation coefficient is employed to perform multiple iterations of similarity measurements between each data point (microarray probeset intensity value) within the vertical axis, thus expression levels between every gene in the data-set. Relationships among genes are represented by a tree, whose branch distance lengths reflect the degree of similarity between genes. This distance can be calculated depending on the amount of constraint needed; as a single-linkage cluster (where Cluster calculates the minimal distance between two genes), an average-linkage (calculates the average distance), or complete-linkage cluster which is the most conservative measurement of gene expression similarity that calculations the maximum distance.

The clustering procedures yield a binary tree where genes are near each other on the tree if they are strongly correlated, and branches of similarly expressed genes group into

discrete nodes. The same algorithm is then applied to cluster the experimental samples according to their overall patterns of gene expression.

A graphic display of the intensities of the genes by individual subjects is then created in the program TreeView (M.Eisen). Intensity of each gene is normalized by median centering and represented by a color scheme varying from red for high intensities to green for low. The genes are ordered along the vertical axis using the binary tree from the first cluster analysis. The subjects are arranged across the horizontal axis according to the second binary tree. This visual representation of the data shows clusters of genes that exhibit similar expression intensity among each individual subject.

Hierarchical clustering is performed on all 40 prostate cancer patients and 20 control subjects recruited during this study. The gene expression data will correctly classify patients from controls. It should be noted that the hierarchical Clustering algorithm will cluster only those genes that exhibit a similar pattern of leukocyte expression among subjects. Thus, differential gene expression that arose, *e.g.*, from an irregular immune response in only one individual will not be included in the cluster of similarly expressed genes among all subjects. Although this may result in some genes being removed from analysis due to variable levels in some subjects, this algorithm will act to reduce the influence of the many non-PCa related gene expression changes that may be detected when analyzing so many data points.

Expression profiles can distinguish prostate tumor samples according to the stage of tumor aggressiveness. The results derived from the clustering algorithms should correlate with tumor stage, *e.g.*, all patients with a defined stage of T3 should cluster together in a sub-node, away from sub-nodes of different staged tumors. To analyze Cluster results all TreeView readout data are compared with the detailed surgical report pathology provided for each patient employed in this analysis to identify clusters of patient samples that fall within similar clinical and pathological tumor stages. Such an approach has been successfully applied to distinguish among populations of both B-cell lymphomas (Alizadeh *et al.*, *supra*), multiple breast tumors (Perou *et al.*, 2000) and prostate tumor tissue (Dhanasekaran *et al.*, *supra*).

It may prove useful to perform a supervised clustering experiment, as this Example employs a surrogate tissue in which differences in the patterns of gene expression of leukocytes from tumor patients may be more subtle than the differences obtained from analysis of the tumor tissue itself. Supervised clustering can be performed using

5 adjustments within the Cluster program. For example, for the initial data analysis each sample was given equal weighting *i.e.*, each sample was assigned equal importance (and thus defined as unsupervised). If the weighting of the samples is altered and the data is then analyzed in Cluster using GORDER, which provides a constraint on the algorithm to keep the samples in particular groups (*e.g.*, groups of prostate cancer patients at disease T2  
10 versus groups of patient at T3), the horizontal axis of gene similarities will be defined by this order. In this instance, branch length within and between nodes can be employed to identify genes with similar expression patterns between the selected groups.

Finally, genes that are significantly differentially expressed between subgroups of patients and/or subgroups of controls (that have not been removed by flagging procedures)  
15 may have strong weighting on the final clustering results. This may alter the final nodes of the clusters and even skew the overall cluster data. Therefore statistical tests, such as the student T-or Wilcoxin test (ensuring that in each instance there are sufficient sample numbers for analysis), are performed to identify, and then remove from analysis, genes significantly differentially expressed between, all control subjects. This procedure should  
20 help to greatly reduce the inter-subject variation.

***Supervised Learning Algorithms.*** Supervised learning algorithms are based on an initial definition of the subject groups to be distinguished by the algorithm. A sub-set of each group is employed to determine characteristics that can separate the two groups, in this case gene expression levels. The characters, or genes, that play a role in the  
25 separation, are then used on a test set of data (the remaining subjects), to call each test sample. Two algorithms employed for this analysis are briefly described below.

***Group Classification.*** Group Classification (Golub *et al.*, 1999; Slonim *et al.*, 1999), has been recently used to investigate genetic differences between leukemia's, elucidating gene expression distinctions between two forms of this disease. This algorithm  
30 will be used to evaluate and compare the results generated through the hierarchical



clustering method. Following procedures employed by Golub *et al.*, (*supra*) subjects are divided into two sets: the “training set” includes 20 prostate cancer patients and 10 normal control subjects; the “test set” includes an additional 20 tumor patients and 10 control subjects. A multigene expression signature is constructed using the 30 subjects from the “training set”, as follows. First, all genes are sorted by the degree of correlation between the expression level and subject diagnosis, in this case being positive or negative for prostate cancer. A correlation metric which measures relative class separation is used [correlation metric  $P(g,c) = (\mu_1 - \mu_2)/(\sigma_1 + \sigma_2)$  where  $g$  = the expression vector of a gene over  $n$  samples and  $c$  = the diagnostic class vector]. The significance levels of these correlations is then determined using a permutation test called “neighborhood analysis” .. Taking the significantly correlated genes, different subsets of genes are then tested to find the best model for classifying diagnosis using cross validation procedures within the “training set”.

The final model is then used with the “test set” of additional patients and controls, to see if subjects can be correctly classified with a positive or negative tumor diagnosis. Each gene “votes” for cancer or normal diagnosis, based on whether its expression level is closer to the mean expression level of prostate cancer patients or of normal controls. This vote is weighted by the degree of correlation between the gene and diagnostic group. Votes across all genes are summed to make a final classification of diagnosis, provided there is sufficient prediction strength as measured by the margin of “victory” [prediction strength =  $(V_{\text{winner}} - V_{\text{loser}}) / (V_{\text{winner}} + V_{\text{loser}})$  where  $V$  is then number of “Votes” received for each diagnosis]. Classification of subjects is evaluated in terms of error rate (% incorrect classifications) and “no-call” rate (% of samples considered “uncertain”).

**Support Vector Machine.** A support vector machine (SVM) supervised learning algorithm has recently been employed to perform multiclass cancer diagnosis of 14 different tumor classes and control tissues, and is employed for analysis of the prostate and control sample leukocyte gene expression data. Data input for this algorithm is similar to group classification, whereby subjects are divided into training and test sets. The training set is then characterized by labeling or classing each subject as positive +1 (*e.g.*, prostate cancer samples) or negative -1 (*e.g.*, control samples). SVM finds a hyperplane,  $w$ , which separates positive and negative training samples and maximizes the margin, or distance,

between the samples and the hyperplane, where  $f(\mathbf{x}) = \mathbf{w} \cdot \mathbf{x} + b$ . The geometric property can be imposed by means of the following optimization problem: minimize  $\frac{1}{2} \|\mathbf{w}\|^2$  subject to  $y_i(\mathbf{w} \cdot \mathbf{x}_i + b) \geq 1$ , for all  $i$  (where  $\mathbf{x}$  is the input data, e.g. expression level;  $y$  is the class label +1 or -1). The discriminate function can be written as  $f(\mathbf{x}) = \sum w_i y_i(\mathbf{x} \cdot \mathbf{x}_i) + b$ ,  
 5 where  $w_i$ 's and  $b$  can be obtained from solving the quadratic function. The hyperplane is then employed for classification of the test set, where an unknown test samples position relevant to the hyperplane determines its class, and the confidence of each SVM prediction is based on (and is proportional to), the distance of the test sample from the hyperplane.

The SVM described above results in a binary classification, which is employed to  
 10 distinguish between the two groups of 40 prostate cancer patients and 20 control subjects. Evaluation of the ability of the algorithm to correctly group patients and controls will determine which genes are major effectors in the classification, and the statistical power of each for each sample.

In the papers referenced above, a one-versus-all (OVA) approach has also been  
 15 employed to perform multiclass prediction. The OVA builds  $k$  (the number of classes) binary classifiers which distinguish one class from all the other lumped together (Yeang *et al.*, 2001; Ramaswamy *et al.*, 2001). For a test sample  $\mathbf{x}$ , the binary classifier outputs form a  $k$ -vector  $f(\mathbf{x}) = (f_1(\mathbf{x}), \dots, f_k(\mathbf{x}))$ . If  $f(\mathbf{x})$  is a real number (*i.e.*, a predicted class with confidence value), then the predictor finds the maximum of  $f_i(\mathbf{x})$  and assigns the  
 20 sample to the corresponding class label. Using this approach, Ramaswamy *et al.*, created a multiclass cancer gene expression database from 144 human cancers and normal tissues from a total of 14 classes, and demonstrated a 78% accurate classification/diagnosis of the correct cancer or control tissue over the set of test samples ( $n=54$ ) (Ramaswamy *et al.*, *supra*). An OVA approach, where  $k$  = each stage of prostate tumor (*i.e.*, T1-3(4)) can be  
 25 employed here.

#### Analysis of Leukocyte Gene Expression and The Multigene Expression Signatures Determined Following Data Analysis

**Quantitative RT-PCR.** Although recent reports have documented the reliability and reproducibility of microarray analysis, this powerful technology is still in its infancy and it may be necessary to perform additional confirmation of the expression results obtained.

Therefore, gene specific primers are designed for a number of genes seen to be

5 differentially regulated among leukocytes obtained from cancer patients and controls, and employed for assay via real-time RT-PCR of leukocyte transcript levels. The actual number of genes employed for validation of results depends on the number of genes found in this assay to be differentially expressed. Microarray experiments performed by other researchers, and cited above, are available as guidelines for this analysis. Genes chosen for  
10 this analysis include those identified in previous studies that are differentially regulated between leukocytes from patients with a solid tumor relative to leukocytes from control subjects (and are thus positive controls), and also genes included in the multigene signatures deduced through the data analysis. For each gene analyzed, RT-PCR analysis is used confirm and validate the outcome of the microarray analysis.

#### 15 **EXAMPLE 4: BREAST CANCER DIAGNOSIS BLOODCELL MULTIGENE SIGNATURES**

##### Introduction

Breast cancer is the second leading cause of cancer deaths in North American women. It has been estimated that in 2002, 203,500 new cases of breast cancer were  
20 diagnosed in the US, with approximately 39,600 deaths in that year alone (Jemal *et al.*, 2002) Current techniques for the screening of breast cancer, as a prerequisite to biopsy for diagnostic evaluation of the detected mass, include physical breast examination and mammography. These techniques possess a number of limitations, including lack of specificity and accuracy in the diagnosis and, also a lack of cancer stage and prognostic  
25 information. This ultimately yields high numbers of false positive diagnoses, and consequently unnecessarily large numbers of surgical biopsies. The rationale behind this proposal is based on two sources of data: 1) Current scientific literature, in which there is growing evidence that individuals with breast cancer and other forms of malignant disease such as prostate cancer, exhibit immune responses that can be detected at the level of  
30 altered gene expression in leukocytes circulating in peripheral blood. Quantitation of the mRNA transcripts in leukocytes of a number of individual genes has demonstrated

associations between gene expression levels and the presence of a tumor in patients with breast and prostate cancer. 2) Preliminary results from a microarray study investigating gene expression changes in men with prostate cancer. Initial results from this study have been striking; supervised cluster analysis of peripheral leukocyte gene expression data, using transcript level measurements of thousands of genes from eleven prostate cancer patients and seven matched control subjects, resulted in a classification of all the subjects into their correct group.

The use of microarray technology allows the simultaneous measurement of the expression levels of up to 14,000 genes transcribed in circulating leukocytes derived from the blood of breast cancer patients and control individuals. This technology, demonstrates that women suffering from breast cancer exhibit a conserved pattern, or signature, of gene expression levels in their peripheral blood leukocytes, which is distinct from the corresponding pattern of expression in leukocytes from control subjects. Patients with breast cancers at different histological grades, yield distinct expression signatures that reflect the biological stage and aggressiveness of the cancer, and that information can thus be employed to differentiate among breast cancers at different pathological stages.

This Example demonstrates a novel technique that does not require invasive techniques to obtain tumor tissue, yet provides an accurate diagnosis of breast cancer, and also provides detailed prognostic information on the stage and biological aggressiveness of the tumor. The success of this project would yield a much needed, non-invasive tool for stage-specific diagnosis of the disease, and thus serve as an important screening tool to identify women with breast cancer.

Although mortality rates have decreased over the past decade, through pre-symptomatic screening programs and major improvement in breast cancer treatment, breast cancer survival rates decrease dramatically in women with a more advanced stage at diagnosis and it has been estimated that only half of all breast cancers are localized at the time of diagnosis. Thus, effective management of breast cancer relies heavily on an early diagnosis, coupled with a need to obtain accurate information on the classification and stage of the cancer itself, and thus limitations of traditional diagnostic and prognostic techniques may currently hinder the management of breast cancer.

Although frequently advocated, evidence to support the use of breast self examinations (BSE) in screening programs is weak. To date, no study has evaluated the effectiveness of clinical breast examinations (CBE) as a stand-alone screening technique. Widespread adoption of screening mammography, which utilizes ionizing radiation to  
5 image breast tissue, has been accredited with the dramatic increase in incidence rates of breast cancer between 1980-1987, illustrating the benefit of screening programs in identifying the presence of breast cancer. However, there has been much recent controversy over the benefits versus the risks of regular mammography (reviewed in Humphrey *et al.*, *supra*). Thus, in large mammography screening programs, for every one  
10 hundred dollars spent on screening thirty three will have been spent on the evaluation of false positive results (Elmore *et al.*, . N Engl J Med. 1998;338(16):1089-96).

Other techniques include the use of ultrasound in the evaluation of palpable or mammographically identified masses, and the use of serum tumor markers for the detection of breast cancer, such as CA15.3, lack sensitivity and specificity (Chan D.W., 2001) and  
15 research has focused on the use of PCR-based approaches for tumor micrometastasis detection. Quantitative RT-PCR analysis of gene products, in malignant cells that have survived detachment from the original tumor site and circulation within peripheral blood, has been employed to identify metastatic disease, and detection of circulating levels of the mRNAs transcribed by the genes CK-19, MUC1, CEA and mammoglobin, has been  
20 reported to provide both diagnostic and prognostic information on breast cancer (Berois *et al.*, Eur J Cancer 2000; 36(6):717-23). However, problems with these methods have been documented such as the detection of CK-19 pseudogenes that can contaminate results, and the lack of replication and lack of tissue specific expression detected following analysis of mammoglobin.

25 Research has implied that some important diagnostic and prognostic information will be derived only after surgical procedures, and in current clinical practice an actual diagnosis of breast cancer is made following pathologic review of a tissue specimen. Breast tissue can be obtained by the methods of excisional or incisional biopsy, where the entire palpable mass or a section of the mass (respectively) is surgically removed. Although  
30 accurate, these techniques are very painful for the patients and lead to extensive scarring (which can mimic a malignancy on physical or mammographic examination).

***Differential Expression Of Individual Genes In Leukocytes From Patients With Breast Cancer.*** The tumor derived antigen 90K (Mc-2 BP) is a widely expressed, secreted glycoprotein found in the serum of healthy individuals. Levels of the 90k protein are significantly increased in the serum of patients with breast cancer, and Fusco *et al.*, showed  
5 that 90K serum protein levels were also elevated in 20% of patients with no clinical evidence of the disease (*et al.*, Int J Cancer. 1998;79(1):23-6). Fusco *et al.*, additionally showed that transcript levels of the 90K gene were also higher in patients versus controls, and they suggest that peripheral blood cell monocytes (isolated from whole blood) may be activated in response to breast cancer growth and progression.

10 Martin *et al.*, performed an targeted microarray based investigation using RNA template derived from blood of breast cancer patients (DCIS to Stage IV), (*et al.*, Proc Natl Acad Sci USA.;98(5):2646-51). Genes were chosen to be placed on the array if they were found to be differentially expressed between breast cancer tissue and control breast tissue by differential display (n=170). Cluster analysis identified a group of 12 genes that were  
15 elevated in 77% of the subjects with more aggressive cancer, including the genes maspin, CD44 and HER2. However, although the authors hypothesize that they are detecting disseminated breast cancer cells (Martin *et al.*, *supra*), they suggest that their results may also arise from the detection of mRNA transcripts within the leukocytes themselves. Evidence to support this alternate hypothesis also comes from preliminary studies measured  
20 leukocyte expression levels were measured in prostate cancer patients and control subjects. The genes *maspin*, *CD44* and *HER2* were all found to be significantly expressed above background levels in all subjects, and *HER2* was shown to be up-regulated in prostate cancer patients. As described above, experiments that show the accurate classification of prostate cancer subject and healthy control subjects into their respective groups, based on  
25 the expression levels of over 1500 gene, provide evidence to support breast cancer diagnosis though leukocyte expression signatures. The genes employed above for classification of prostate cancer will not necessarily be the exact genes employed for classification of breast cancer. However, extensive literature has been published documenting the common similarities between breast and prostate cancer, including  
30 incidence and mortality rates, risk factors, initiation of transformation, and roles of androgens and estrogens (reviewed in Lopez-Otin & Diamandis Endocr Rev. ;19(4):365-

96). These data, along with results presented *infra*., provide evidence that growth and development of a breast cancer will exert an effect on the immune system that can be detected at the level of altered gene expression in peripheral blood leukocytes.

5 This Example employs microarray technology to quantify mRNA transcripts, which allows the simultaneous analysis of thousands of genes expressed in peripheral blood leukocytes. The complex differential gene expression measured using this approach identifies patterns or signatures of gene expression that differ between breast cancer patients and control subjects, and thus forms the basis of a diagnostic technique.

10 It seems clear that the use of multiple gene products for the determination of expression signatures provides considerably more detailed information on tumor stage and prognosis than can be provided by the quantitation of individual serum protein levels. It should also be noted that although leukocyte gene expression levels will be measured, if, *e.g.*, malignant breast cells were also present in the blood of patients, then gene expression of these cells will also be quantified. It seems likely that the detection of gene expression  
15 in malignant cells within blood would actually increase the specificity of this analysis, as mRNA levels arising from circulating metastatic cells would differ from mRNA levels in patients with no metastatic cells in their blood stream.

Affymetrix oligonucleotide microarray technology is employed to simultaneously measure the expression levels of up to about 14,000 genes transcribed in circulating  
20 leukocytes derived from the peripheral blood of 55 breast cancer patients and 25 control individuals as described above. In a specific experiment, leukocytes are collected and subjected to sample processing and microarray hybridization. Expression data derived from microarray hybridization plus data-analysis algorithms to generate multigene expression patterns is used for analysis.. These data show that circulating blood leukocytes  
25 in individuals suffering from breast cancer exhibit a characteristic signature of gene expression levels that is different from the signature exhibited by circulating leukocytes from control subjects. Multigene expression signatures in individuals with breast cancer are specific to the aggressiveness of the tumor from the individual examined, and thus reflect the stage the malignancy has reached in the patient.

### Materials And Methods

**Breast cancer subjects.** The experimental approach measures leukocyte gene expression levels in 55 breast cancer patients, and 25 matched control subjects, with duplicate sample processing of each subject. Duplicate processing was performed to permit the robustness of a cancer-specific gene expression signature to be determined. The microarray technology and pattern analysis algorithms and analysis are the same as for the prostate study in Example 3.

All breast cancer patients are potential candidates for enrollment into this study, and this total population of breast cancer patients is screened for possible recruitment into this study. Informed consent is obtained, according to Institutional Board Regulations. Blood drawing takes place following initial diagnosis or confirmation of breast cancer diagnosis, and prior to the onset of treatment for the disease. Treatment options for breast cancer are generally directed by the stage that the tumor has reached in that individual. For example, treatment for Stages I and II most often involves a combination of surgery and radiation therapy and/or adjunct systemic therapy. Treatment for stage III, which is characterized by lymph node involvement, may alternatively start with chemotherapy, followed by surgery and radiation therapy. Patients from stages I, and II, and stage III will be included only if recruitment and blood drawing was performed prior to the initiation of therapy. Additionally, patients with advanced metastatic disease may also be recruited if they are screened for participation prior to the onset of treatment for localized and metastatic disease.

Annual estimates of patients available at stages I, II, and III are about 80-100. It is not contemplated to specifically screen and exclude patients based on actual tumor stage, or the presence of metastatic disease. This broad inclusion should allow recruitment of at least 20 patients from stages I-III.

Each patient recruited to participate in this study is provided with a questionnaire designed to obtain both demographic information and information on current general health. The questionnaire is approved by the Institutional Review Board. Clinical information, biopsy reports (including dates of biopsy), and any further pathology reports are also collected for this study. This documentation includes all patient history, all results of any



mammography, ultrasound, and core needle biopsy. CBCs is performed on all recruited patients following blood drawing.

***Exclusion Criteria for Patients.*** Patients will be excluded from this study if: 1) they have had surgery or other physical trauma less than six weeks prior to blood collection, 2) if they have abnormal CBCs, 3) if they have a current infection, 4) if they have autoimmune disease, 5) if they have had chronic use of immunosuppressants or anti-inflammatory medication. These exclusion criteria have been designed to reduce the likelihood of including breast cancer patients that exhibit leukocyte gene expression that is different from healthy control subjects, but that arises from factors other than growth and development of a breast cancer, such as an immune response to surgery or the presence of an infectious agent.

***Control subjects.*** Twenty-five control female subjects, approximately age-matched to breast cancer patients, are recruited from the staff and staff relatives. Informed consent is obtained, according to IRB regulations. Each control subject recruited to participate in this study is provided with a questionnaire to obtain both demographic information and information on current general health. The questionnaire is approved by the Institutional Review Board. Information collected through the completion of this questionnaire is employed as described, as well as to determine that a control subject is unlikely to have an undiagnosed breast, or other solid tumor, that may effect leukocyte gene expression. Blood samples are drawn by a trained phlebotomist from the antecubital vein using a needle and evacuated tube. For each control subject chosen to take part in this study, CBC counts are performed. Clinical Breast Examinations for control subjects are also performed. Control subjects are informed, in writing, of the results of their CBE.

***Exclusion Criteria for Controls.*** Control subjects are excluded from this study if: 1) they have abnormal CBCs, 2) they have a high risk factor for developing breast cancer, such as two first-degree relatives with the disease, 3) if they have a first-degree relative diagnosed any other solid tumor, 4) if they have documented a current infection, 5) if they have autoimmune disease, 6) if they have had surgery or other physical trauma less than six weeks prior to blood collection, 7) if they have had chronic use of immunosuppressants or

anti-inflammatory medication. Control subjects are excluded if a palpable mass is detected by CBE.

***Potential Problems Arising from Factors Other Than Breast Cancer.*** During recruitment of both breast cancer patients and control subjects, it is clear that attention must be paid to the possibility that the mRNA levels of some of the genes expressed in leukocytes, in both patients and control subjects, may change because of underlying inflammatory disease states or other illness. As described above, both breast cancer patients and control subjects are otherwise normal healthy individuals with no history of autoimmune disease or current infection. It is unlikely that any control subject has an undiagnosed breast carcinoma or other solid tumor.

However, it is well known that individuals possess different immune complements, and these may well be detected within these experiments. Flagging is a method employed to normalize between patient samples and this will be employed to reduce some of the inter-subject variability that may be detected following microarray hybridization. Any gene found to be significantly differentially expressed ( $> 3$  fold change) between two or more of the normal control individuals, will be “flagged”, which subsequently removes this gene from any further analysis. This method was successfully used to remove inter-subject variation from both multiple patient samples such as total lymph nodes, and also from multiple cell lines of different lineages that were employed to identify profiles of gene expression in B cell lymphomas (Alizadeh *et al.*, Nature 2000; 403(6769):503-11). It should be noted that however that this approach to remove gene expression variability, or “noise”, was not employed in the preliminary studies, as supervised hierarchical clustering analysis was performed, where expression noise can be removed from the data set prior to input into the data analysis algorithms. Furthermore, flagging genes may eliminate too many genes from analysis. With this in mind, expression analysis is performed on the data sets pre- and post-flagging.

The algorithms described in detail below have been successfully employed to identify gene expression profiles that distinguish complex tumor tissue from normal non-disease tissue (that has not undergone micro-dissection procedures), and thus are not hindered by complex patterns of total gene expression.

**Use of the Affymetrix Oligonucleotide Microarray Technology.** The Affymetrix system appears to be better suited to the present project than a cDNA microarray-based system. Therefore, Affymetrix Human Genome U133A oligonucleotide microarrays are employed to analyze gene expression signatures in peripheral blood leukocytes taken from the breast cancer patients described above, and in corresponding cells from control subjects recruited during this study. This array is an upgraded version of the HU95A arrays employed in the preliminary studies, and will soon replace this array. The arrays are comparable with each other.

Affymetrix Human U133A oligonucleotide microarrays contain about 14,000 individual human sequence verified oligonucleotides, representing Unigene, GenBank and TIGR database clusters that have been previously characterized by function and disease association. The specific gene products described above are all represented on this microarray and thus are included in all analytical procedures. Furthermore, many other genes known to be involved in immune responses are also included on this microarray, such as multiple cytokines and growth factors, and *e.g.* maspin, which has been found to be down-regulated in breast cancer mouse models.

***Sample Processing, Probe Preparation and Microarray Hybridization.*** All blood samples are processed immediately following collection; leukocytes are extracted from blood using lysis buffers and centrifugation, according to standard procedures. The storage of leukocytes at that temperature allows the retrospective determination of which samples are to be hybridized to GeneChips, after a detailed analysis of all available patient history and a confirmed histological analysis of biopsy samples (and tissue, in the case of patients undergoing surgery after their participation in this study). All patient and control samples chosen for RNA extraction are then processed in duplicate, by splitting the white blood cell sample extracted from whole blood and processing the duplicate samples identically thereafter.

***Replicate Sample Processing Versus Non-Replicates.*** The need for replicate microarray experiments has been previously highlighted (Lee *et al.*, 2000). There is much discussion in the scientific community on the need for replication, and biostatisticians have suggested that a lack of replication will restrict the use of formal statistical tests. Sources

of variation and necessary levels of replication vary considerably among the array platforms to be employed, however Dudoit *et al.*, have suggested that many considerations on replication are applicable to both cDNA and oligonucleotide platforms ( Statist. Sinica. 2000; 12, 111-139).

5           The term biological replication can have two meanings; “actual biological replication” is the replication of array processing and hybridization involving mRNA from different extractions from the same sample or individual, and “biological replication”, where target mRNA comes from, *e.g.*, different version of a cell line, or different individuals. These forms of replication are very different in nature, with the latter  
10 involving a much greater degree of variation in measurements (Yang *et al.*, Nat Rev Genet. 2002; 3(8):579-88). For the efficient design of this study the choice of biological replication is very important. For example, it may be that variation between individuals will be larger than other sources of variation (*i.e.* experimental), and thus it may be inefficient to perform replicate arrays from a small number of samples. However, Simon *et*  
15 *al.*, Genet Epidemiol. 2002; 23(1):21-36, have suggested several motivations for performing actual biological replication, as this replication provides an estimation of the reproducibility of the experimental procedures, it permits the identification and discarding of “bad” arrays, and actual biological replication can improve precision of the estimate of the expression profile for a given RNA sample though the averaging of multiple arrays.  
20 Furthermore, replicate samples are extremely useful when attempting to establish that a classification between diseases is robust, which is particularly true for class discovery algorithms, where the large number of genes make it relatively easy to discover interesting patterns of gene expression, even in random datasets.

          The Affymetrix system provides a significantly lower variation between  
25 experiments, suggesting that the need for 3 or more replicates can be reduced. Additionally, each sample is processed in duplicate, thus performing actual biological replications. The above considerations, in particular that the robustness of the classification is deemed essential, coupled with the frequently reported use of duplicate hybridizations in Affymetrix oligonucleotide array experiments, and the use of actual biological replicates in  
30 two landmark papers on identification of breast cancer expression profiles (Perou *et al.*,

Nature 2000; 406(6797):747-52; Van t'Veer *et al.*, Nature 2002;415(6871):530-6) justifies the use of duplicate sample processing.

**Data Analysis.** All data analysis is performed as described for prostate cancer expression profiling in Example 3.

5       **Analysis of Leukocyte Gene Expression and the Multigene Expression Signatures  
Determined Following Data Analysis**

10       *Quantitative RT-PCR to Confirm the Results of the Microarray Experiments.* For validation of microarray results, primers are designed to amplify a number of genes seen to be differentially regulated among leukocytes obtained from breast cancer patients and  
15       controls, and employed for assay via real-time RT-PCR of leukocyte transcript levels. The actual number of genes employed for validation of results depends on the number of genes found to be differentially expressed. Microarray experiments performed by other researchers, and cited above, are available as guidelines in determining the number of gene that need to be analyzed to validate the microarray results. Genes chosen for this analysis  
20       include those identified in previous studies that are differentially regulated between leukocytes from patients with a solid tumor relative to leukocytes from control subjects (and are thus positive controls), and also genes included in the multigene signatures deduced through the data analysis. For each gene analyzed, RT-PCR analysis is used to confirm and validate the outcome of the microarray analysis.

**EXAMPLE 5: PSYCHIATRIC ILLNESS WITH MULTIGENE EXPRESSION CLASSIFICATION**

5

**Introduction**

Previous studies have shown associations between white blood cell (leukocyte) gene expression levels and the psychiatric disorders bipolar disorder (BPD) and schizophrenia (SZ). As shown in the Example above, patients with SZ have a characteristic leukocyte multigene expression pattern or signature that differs from healthy control subjects. The positive expression data results collected for schizophrenics (n= 8) and healthy controls (n= 5), in addition to the contrasting gene expression differences reported between healthy controls, and patients with BPD or SZ [Spleiss *et al.*, Mol Psychiatry 1998; 3,512-20; Ilani *et al.*, Proc Natl Acad Sci U S A 2001; 98(2), 625-628)], establishes that specific leukocyte multigene expression profiles can differentially classify psychiatric illness.

This Example generates gene expression data from patients with BPD and SZ. The data create classifying multigene expression profiles for each of the disorders, using hierarchical clustering and supervised learning algorithms, that can be used to correctly distinguish leukocyte samples taken from patients with either BPD or SZ. This in turn leads to improved treatment targeting for patients with BPD and SZ, following classification with multigene expression profiles. This work also establishes the ability to define those at risk for the development of BPD and SZ based on the multigene expression signatures.

**Rationale**

The psychiatric disorders to be investigated during this proposed study, BPD and SZ, have incidences in the general population of approximately 1%. Susceptibility to these disorders includes a large but variable genetic component, and there are efforts currently underway to find genes that play roles in the development of the diseases, through linkage analysis and association studies. Several chromosome regions and genes have been suggested as candidates for disease loci (Tsai *et al.*, J Affect Disord 2001; 64,185-93; Cloninger *et al.*, Am. J. Med. Genet. 1998; 81,275-281). Physical, biological and

environmental factors such as birth trauma low birth weight, poor fetal nutrition, viral infection, autoimmune processes and winter/spring birth are also thought to contribute to the risk of developing BPD and SZ, as they may impact the developing brain either *in utero* or during postnatal development [Kinney *et al.*, J Affect Disord 1998; 50,117-24; Gunduz  
5 *et al.*, Schizophr Res. 1999; 40,237-433). There are currently no genetic or biochemical markers or tests which can specifically predict the onset of these psychiatric illnesses or differentiate between the disorders.

A biological assay providing information that could help classify BPD and SZ, and define susceptibility at an early stage, especially in high risk families, may allow targeted  
10 treatment strategies to commence before the onset of many symptoms.

There is a growing literature illustrating the usefulness of global gene expression measurements in the characterization and classification of diseases and their subtypes, such as prediction of patient survival time, and response and sensitivity to treatment (see e.g., Sorlie *et al.*, Proc Natl Acad Sci U S A 2001; 98,10869-74 In parallel to the above  
15 Examples, and of interest to this Example, Hoffman *et al.* recently described the first disease classification, by microarray analysis of brain tissue, between Rett syndrome patients and controls (Colantuoni *et al.*, Neurobiol Dis. 2001; 8,847-65).

To date, published microarray analyses of samples from patients with SZ and BPD have focused on analysis of post mortem brain tissue to investigate their etiologies . Upon  
20 microarray analysis of prefrontal cortex, one group has suggested SZ is a disease of the synapse, and that expression analysis of genes involved in the regulation of presynaptic function may elucidate different sub-types or etiologies of SZ (Mirnics *et al.*, Trends Neurosci, 2001; 24,479-86). The results of a study employing Affymetrix GeneChips showed altered expression of genes involved in different functions, such as myelination,  
25 again providing detailed data on biological processes in the brain of SZ patients.

Although microarray analysis of brain samples has, and will provide important information on the etiology and pathogenesis of BPD and SZ, it is obvious that use of brain samples from living patients for molecular diagnostic classification is not feasible. Thus, the development of any multigene expression-based classification of BPD and SZ should  
30 focus on a tissue that is accessible. Peripheral blood samples are easily obtained and most

significantly, it has previously been reported that SZ and BPD patients have altered levels of multiple gene products that are expressed in blood leukocytes. In a recent report, Ilani *et al.* measured the mRNA levels of the Dopamine D3 receptor gene in leukocytes from SZ patients and matched control subjects. They demonstrated that in SZ patients, transcripts of the D3 receptor were significantly elevated, and that this 2-3 fold increase in expression was not affected by antipsychotic drug treatments (typical or atypical).

Moreover, non-medicated SZ patients were found to exhibit the same patterns of gene expression, suggesting that drug treatment itself does not effect gene expression of the D3 receptor in peripheral blood leukocytes (PBLs). A similar study performed on a larger patient population both confirmed the above observation and suggested that measurement of D3 receptor mRNA may also be useful in the classification of symptom severity subgroups (Kwak *et al.*, BMC Med Genet. 2001; 2(1):3).

Although an early report using post mortem brains described a decrease in D<sub>3</sub> receptor levels in SZ brains when compared to brains from control subjects, more recent studies have suggested that in some areas of the brain the D<sub>3</sub> receptor levels are increased in non-medicated SZ patients, and that the elevation is reduced by neuroleptic medication (Joyce *et al.*, Ann N Y Acad Sci. 1999; 877,595-613).

Decreases in levels of D<sub>3</sub> receptor mRNA in PBLs have been observed in Parkinson's disease compared to controls. with similar down-regulation of D<sub>3</sub> receptor in Parkinson's brains (Guillen *et al.*, Nature 2001; 411,86-9, while in Alzheimer's disease (AD), a reduction of PBL dopamine D<sub>2</sub>-like receptors was reported (Barbanti *et al.*, Mech Ageing Dev 2000; 120,65-75. , consistent with the levels of D<sub>2</sub>-like receptors in brains of AD patients, compared to control subjects. The studies lend support to use of surrogate peripheral markers in classification of psychiatric/neurological disorders, although the question remains, whether peripheral markers simply reflect brain expression levels, or alternatively may have functions in disease processes. Interestingly Levite *et al.* concludes from a recent study, that dopamine receptor levels on human T-cells actually reflect increased/decreased lymphocyte functionality, and report their observations that upon stimulation by a dopamine receptor agonist that mimics the effect of dopamine, the D<sub>3</sub> receptor expression on T-cells is stimulated and results in the further activation of T-cell function (Eur J Immunol. 2001; 31,3504-12).



A study of leukocyte inositol monophosphatase (IMPase) mRNA from BPD patients and control subjects showed decreased expression in BPD, with the greatest decrease observed in non-drug treated patients (Nemanov *et al.*, Int J Neuropsychopharmacol. 1999; 2,25-29). Additionally, a measurement and comparison of leukocyte G protein alpha subunit mRNAs in BPD patients compared with mRNA levels in unipolar patients and control subjects, showed a significant increase of transcript levels in the BPD group compared to both other groups (Spleiss, *supra*).

Results from previous studies of BPD and SZ show alterations in the concentrations of immune response mediators in blood. There also appear to be differences between the disorders in the profile and magnitude of IRS mediator changes compared to control subjects, with the literature including instances of increased serum soluble Interleukin-2 (IL-2) receptor in BPD. In SZ there is further evidence to suggest the presence of altered leukocyte gene expression (*see e.g.*, Lin *et al.*, Schizophr Res. 1998; 32(1), 9-15), and although there are contradictory findings and some reports suggesting that neuroleptic medication may confound these studies by causing alterations in IRS markers, the majority of the studies using neuroleptic naive or non-medicated SZ patients show IRS activation in SZ. IRS gene products reported to be up-regulated in blood from SZ and BPD patients, and that are represented on the microarrays that will be utilized in the proposed study include; IL-6, IL-1 receptor antagonist (Akiyama *et al.*, Schizophr Res. 1999; 37(1), 97-106., IL-2 and IL-2 receptor (Tsai *et al.*, *supra*). CD4, CD8, CD4/CD8 ratio, CD3 (as measured by levels of CD+ cells in blood samples) [66;67] and TNF- $\alpha$ . VLA-4 receptor expression on CD4+ and CD-8+ T cells was also found to be increased in SZ, and differential regulation of the IRS-associated HSP-60 and HSP-70 have been observed in patients with SZ.

Most recently Tang *et al* have used a rat model to show global gene expression changes in leukocytes, that result from experimentally induced ischemic strokes, hemorrhagic strokes, sham surgeries, kainate-induced seizures, hypoxia, and insulin-induced hypoglycemia (Ann Neurol. 2001; 50,699-707). The specific and characteristic patterns of multigene expression observed for each experimental state lends supports to the paradigm of "surrogate markers", where a pathological insult or process may be confined to a particular organ or process, but can induce a characteristic alteration in the overall

expression profile of circulating leukocytes, thereby demonstrating that medical and neurological diseases can cause disease-specific changes to gene expression in leukocytes.

Example 2, *supra*, reports that men with SZ exhibit a characteristic pattern of leukocyte gene expression that differs from the gene expression pattern of healthy control subjects, and is diagnostic for the disease. This preliminary study generated very encouraging positive data demonstrating that eight SZ patients exhibit a leukocyte gene expression pattern that differentiates them from five healthy controls subjects. Two BPD patients were also analyzed and were shown to cluster into a subnode of the tree diagram discreetly from the SZ subjects. However, the preliminary study involved microarray gene expression analysis of only a small number of SZ (n=8), BPD (n=2), and control subjects (n=5). This Example analyzes 25 male BPD and 25 male SZ subjects.

Although it has been suggested that the expression of single genes could be employed for the diagnosis of psychiatric disorders such as SZ, it seems clear that the measurement of multiple gene products as markers of disease provides considerably more detailed information for diagnosis and thus a more robust classifier than single marker analysis. Significantly, Hakak *et al.*, showed a marked improvement in the separation of SZ subjects from control subjects when many brain markers were employed for analysis (n=35), compared to analysis of few markers (n=6), following linear discriminant analysis (Hakak *et al.*, Proc. Natl Acad Sci U.S.A. 2001; 98: 4746-51).

## Research Design and Methods

**Overview.** Microarray analysis measures the expression of leukocyte samples from 25 BPD and 25 SZ male patients between the ages of 25-60. Subjects are recruited from the residents of a psychiatric center and four community residential facilities. Gene expression data from the proposed study is analyzed employing hierarchical clustering, and supervised learning algorithms, and expression classifying signatures are identified (Ramaswamy *et al.*, Proc Natl Acad Sci U S A 2001;98(26):15149-54; Golub *et al.*, Science; 286(5439):531-7).

**Subject groups.** Male White and African American SZ and BPD subjects are recruited into this study.

**Medication Profiles of BPD/SZ Subjects.** The BPD/SZ subjects recruited for this study primarily suffer from severe illness. In the primary study facility: (a) the SZ patient population comprised approximately, 35% paranoid, 35% residual and 20% disorganized SZ; (b) The BPD patients comprised approximately: 20% DSM 296.40 (most recent episode  
5 hypomanic), 15% DSM 296.44 (most recent episode manic, severe with psychotic features), 30% DSM 296.60 (most recent episode mixed, unspecified), 20% DSM 296.64 (most recent episode mixed, severe with psychotic features) and 10% DSM 296.80 (BPD NOS). Close to all of the patients were treated with neuroleptics during their admissions.

**Subject Recruitment and Diagnosis.** Patients are chart screened for eligibility. For  
10 patients interested in participating, informed consent is obtained in accordance with IRB regulations. Diagnostic interviews using the SCID will be conducted. The Brief Psychiatric Rating Scale (BPRS) (Overall *et al.*, Psychol Rep. 1962; 10,799-812) Clinical Global Impression (CGI) Mini-Mental State Exam (MMSE) (Folstein . J Psychiat Res. 1975, 12,189-198), Scale for the Assessment of Negative Symptoms (SANS) [20-22], and  
15 Scale for the Assessment of Positive Symptoms (SAPS) will be conducted by the Research Nurse and the Psychiatrist C.I. at the patient's ward or residence.

**Medical and Psychiatric Assessments and Exclusions.** Chart records of patient subject's medical examinations including the admission examination is assessed. Medical and psychiatric history information is requested from facilities for all previously recorded  
20 admissions, for the purpose of defining a lifetime psychiatric diagnosis and to determine medical eligibility for the study. A lifetime medication history for each patient is also generated from hospital charts and records requested from other facilities.

A list of medical exclusions at the chart level has been generated and includes current or recent- infectious diseases, autoimmune diseases, proliferative disorders, and  
25 recent physical trauma or surgery, and chronic immunosuppressant or anti-inflammatory medication use.

**Blood work.** As part of the study procedure, CBC counts with differentials. CBC white cell counts outside of normal reference ranges, and clinically significant abnormal SMAC values or thyroid function test values will be used as exclusions.

**Drugs screening.** Results from urine screening for drugs of abuse including marijuana, cocaine, stimulants, barbiturates and heroin, performed at the time of admission are examined. Patients who test positive and those who refuse to be tested are excluded from the study. All subjects are also questioned about cigarette smoking; number  
5 smoked/day and years of smoking are recorded. Alcohol intake and drug abuse history are also recorded.

**Sample Collection.** Fifteen ml blood samples are drawn from the antecubital vein by a study team research nurse at the patient's ward or residence. Bloods are processed immediately to isolate and purify leukocytes.

10 **cRNA Synthesis and GeneChip Hybridization.** High density Affymetrix GeneChip arrays were used in preliminary studies due to: 1) the large numbers of gene sequences represented within the array, 2) the highly developed protocols for probe preparation and microarray hybridization, and 3) the built-in multiple internal standards, plus custom  
15 designed normalization software for accurate comparison of results between each individual hybridizations. This latter point is of great importance, since the experimental plan involves a direct comparison between individual microarray experiments. Affymetrix Human U133A microarrays, which contain sequence-verified oligos representing nearly 20,000 individual genes, are employed to analyze gene expression signatures in blood  
20 leukocytes from the SZ and BPD subjects recruited during this study. This array is an upgraded version of the HU95A arrays employed in the preliminary studies. Both arrays contain all genes described above, and the arrays are comparable with each other. All blood samples are processed immediately following collection. All subjects samples chosen for RNA extraction are processed in duplicate, by splitting the leukocyte sample extracted from whole blood and processing them identically thereafter.

25 **Replicate Sample processing.** The need for replicate microarray experiments is axiomatic. Sources of variation and necessary levels of replication vary considerably among the different array platforms, however Churchill has suggested that many considerations are applicable to both cDNA and oligo platforms. The term biological replication can have two meanings; "actual biological replication" is replication of array processing and  
30 hybridization, involving mRNA from different extractions from the same sample or

individual, and “biological replication” where target mRNA comes from different versions of a cell line, or different individuals. These forms of replication are very different in nature, with the latter involving a much greater degree of variation in measurements.

Several reasons for performing actual biological replication have been suggested; this

5 replication provides an estimate of the experimental reproducibility, it permits the identification of “bad” arrays, and actual biological replication can improve precision of the expression profile for a given RNA sample though the averaging of multiple arrays.

Replicate samples are also extremely useful when attempting to establish that a disease classification is robust, which is particularly true for class discovery algorithms where the

10 large number of genes make it relatively easy to discover interesting patterns of expression, even in random datasets. Each subject was processed in duplicate, and perform actual biological replications. The above considerations, in particular that the robustness of the classification is deemed essential, coupled with the reproducibility of Affymetrix arrays, hybridization protocols and scanning (mean  $r^2=0.967$  for repeat experiments justifies the

15 use of duplicate sample processing.

**Data Analysis.** Affymetrix Software Suite is employed for image acquisition and normalization of the fluorescent signals. Analysis of signal intensities over each probeset within each experiment will fall into two main categories; Hierarchical Clustering (see e.g.,

20 Alizadeh *et al.*, Nature 2000; 403(6769):503-11) and Supervised Learning Algorithms (Ramaswamy *et al.*, *supra*). In addition, group difference testing is performed using SAS GLM procedures, including multivariate analysis of variance (MANOVA), used to test factors such as smoking status and medications as confounds in the group analyses.

Finally, in the preliminary analysis a permutation analysis was employed to assess the subject cluster reliability. A Bootstrapping Cluster analysis will be implemented for

25 reliability investigations.

**Hierarchical Clustering.** A hierarchical clustering algorithm Eisen *et al.*, Proc Natl Acad Sci. 1998; 95(25):14863-8), has been successfully applied to classify gene expression data (Alizadeh *et al.*, *supra*), and is described in Example A, *supra*. Specifically, a Student’s two-tailed t-test is performed across the genes expressed in the subjects

30 leukocytes, and then employed Cluster to perform a supervised analysis on the genes found to be differentially expressed ( $p<0.1$ ), resulting in firstly a classification of SZ and control

subjects into their respective groups, and then a classification of BPD from SZ subjects. For this Example, these and other analysis of variance procedures are used for supervised cluster analysis of SZ and BD. The resultant clusters will represent multigene expression signatures specific for the diagnosis and that are useful for testing classification.

5           ***Supervised Learning Algorithms.*** Supervised learning algorithms are described in detail in Example A, *supra*.

***Validation Using Quantitative RT-PCR.*** Microarray data are validated by real-time RT-PCR on genes randomly chosen from those observed to be differentially regulated among leukocytes obtained from psychiatric patients. Gene-specific primers are designed  
10 and employed for the SYBR Green PCR assay. Specifically, reverse transcribed cDNA is processed in duplicate from each patient RNA sample. Real-time PCR assays are then performed in triplicate for each cDNA sample. This experimental replication allows accurate confirmation and validation of the expression data from microarray analysis.

***Additional Approach to the Development of Multigene Expression Signatures.*** The  
15 Affymetrix GeneChip human U133 series contains a second U133B array, with an additional 15,000 oligo sequences derived from characterized genes and non-redundant EST sequences. Use of this second array may extend the analysis with the aim of increasing the complexity of leukocyte specific multigene signatures.

          This Example results in the creation of leukocyte multigene expression signatures  
20 that can classify leukocyte samples by the patient diagnostic groups (BPD and SZ), and that can be used to predict the class of unknown samples. Recruitment of additional patients from the subject groups ultimately allows the power of the expression signatures to be calculated. SZ and BPD- specific expression multigene expression signatures can be generated from multiple racial groups and female subjects, and further studies can  
25 determine the ability to assess or predict patient response to treatment based on leukocyte multigene expression signatures measured at admission, and/or by collection of longitudinal expression profile data following patient admission and during treatment, to determine correlates of treatment response. A longitudinal study of families with members at increased risk of developing psychiatric disorders because of illness in other family  
30 members can be performed. Gene expression patterns can be detected that classify

psychiatric patients by diagnosis, are present in premorbid/prodromal subjects, and establish whether it is possible to predict risk of psychiatric illness from prodromal samples, potentially allowing for targeting of treatment to at-risk individuals such as those with schizotaxia. Disease-specific classification of psychiatric illness has multiple clinical uses, such as a diagnostic support to the psychiatrist on initial presentation of the patient. Also of major importance for psychiatric genetics research, multigene signatures can be employed to assay members of large SZ and BPD pedigrees employed for genetic linkage studies. Affected members, having an accurate biological classification of diagnosis, may help to avoid compounding errors in linkage studies.

**EXAMPLE 6: SCHIZOPHRENIA DIAGNOSIS WITH LEUKOCYTE MULTIGENE SIGNATURES**

This Example generates gene expression data from neuroleptic naive schizophrenic patients, in order to avoid the potential confounder of neuroleptic drug-derived gene expression changes. Additionally, an increased number of chronic neuroleptic-treated schizophrenics and healthy control subject's cases are tested in the gene expression dataset. The data generated in this proposed study, along with previously collected data, permit classifying multigene expression profile, using hierarchical clustering and supervised learning algorithms, that can correctly distinguish leukocyte gene expression levels of schizophrenic patients from control subjects. This in turn provides diagnostic information from leukocyte multigene signatures and defines those at risk for SZ development. This also establishes the ability to develop multigene expression signatures for other psychiatric disease.

**Background**

Example 2, *supra*, generated very encouraging positive data demonstrating that SZ patients exhibit a leukocyte gene expression pattern that differentiates them from controls.

However, this study involved microarray gene expression analysis of only a small number of schizophrenic patients (n=8) and control subjects (n=5). This Example analyzes 32 male schizophrenic patients and 14 control male subjects, from multiple ethnic groups. Furthermore, the eight schizophrenic patients analyzed in the preliminary study had medication profiles that were diverse and included several different classes of atypical

and typical neuroleptic medications: **Subject 493:** Olanzapine, Depakote, Risperidone.,  
**Subject 494:** Chloral Hydrate, Zyprexa., **Subject 495:** Loxapine, Benztropine, Seroquel,  
Vistaril., **Subject 535:** Clozapine, Artane., **Subject 588:** Haloperidol, Haloperidol  
Decanoate, Cogentin, Depakote., **Subject 630:** Olanzapine, Risperidone., **Subject 631:**  
5 Haloperidol, Clozapine. There is growing evidence supporting disease specific alterations  
of leukocyte gene expression in SZ, but it has also been shown that neuroleptic medications  
can disturb IRS mediator concentrations in blood (Muller *et al.*, Eur Arch Psychiatry Clin  
Neurosci 1997; 247: 308-13) ].

10 In order to prove the presence of a signature, this Example performs the multigene  
expression analysis of neuroleptic naive schizophrenics, employing data analysis algorithms  
that identify common gene expression signatures between naive, and medicated SZ  
subjects, that can be utilized for classification of SZ subjects from healthy control subjects.

**Measurement of Multiple Markers.** Although it has been suggested that gene  
expression could be employed for the diagnosis of SZ using a single marker (Ilani *et al.*,  
15 *supra*)], it seems clear that the measurement of multiple gene products as markers of SZ  
provides considerably more detailed information for identification of the disease and thus a  
more robust classifier than single marker analysis. Significantly, Hakak *et al.*, *supra.*,  
showed a marked improvement in the separation of SZ subjects from control subjects when  
many brain markers were employed for analysis (n=35), compared to analysis of few  
20 markers (n=6), following linear discriminant analysis. The use of multiple markers may in  
future also, *e.g.* allow the classification of biological subgroups of schizophrenic patients  
who respond to different treatments.

mRNA levels quantified by RT-PCR techniques is extremely time-consuming if  
many genes are analyzed in one experiment. By employing microarray technology, mRNA  
25 levels of thousands of genes expressed in peripheral blood leukocytes can be quantified,  
including genes coding for all of the markers described above. Global differential gene  
expression measured using the microarray approach identifies patterns or signatures of gene  
expression that differ between schizophrenic patients and control subjects, and thus form  
the basis of the diagnostic technique.



### Research Design and Methods

**Overview.** Microarray analysis measures the expression of leukocyte samples from 20 neuroleptic-naïve SZ patients, 12 medicated SZ patients and 14 age-matched control subjects. Neuroleptic naïve subjects are recruited from an urban emergency room. The study team clinical staff obtains informed consent, and a 15 ml blood sample is collected from each subject prior to a first neuroleptic dose. Blood samples are processed to isolate and purify the leukocytes and the samples are then stored. Patient notes and admission and discharge diagnoses are reviewed by the study team after twelve weeks, and samples from patients who have a confirmed SZ diagnosis will be further processed for microarray expression analysis. Neuroleptic-treated SZ patients are recruited from the residents of a psychiatric facility or community residential facilities. Control subjects are recruited from the staff. Gene Expression data from the proposed study are collated with the existing preliminary study data, and analyzed employing analysis of variance procedures, hierarchical clustering, and supervised learning algorithms.

**Neuroleptic-Naïve Schizophrenic Patients.** Twenty neuroleptic naïve SZ patients between the ages of 21-65 are completed during this study. Patients presenting at an ER are screened for inclusion in the study. It is estimated that up to about 50% of the neuroleptic naïve subjects initially considered to have SZ and recruited into this study, may later be diagnosed as having disorders other than SZ. Potential subjects are thus recruited and blood samples drawn but not processed to completion until retrospective formal diagnosis by the study team.

Subjects are recruited based on their initial psychiatric evaluation performed by a resident psychiatrist and nurse. For patients interested in participating, informed consent is obtained in accordance with regulations. The neuroleptic naïve status of candidate patients is ascertained from a combination of sources including patient's report of their own status, and other significant sources such as patient's family member reports, and/or psychiatrist or therapist reporting from private care or if they have been outpatients at other facilities, and other collateral information. Patient's initial medical examination information is used to determine general health. Medical exclusion information for this study are ascertained by questioning of the subject and from family members and/or other collateral information. Medical exclusions include current or recent- infectious diseases, abnormal CBC counts,

autoimmune diseases, proliferative disorders, and recent physical trauma or surgery, chronic immunosuppressant or anti-inflammatory medication use.

***Retrospective Neuroleptic-Naive Subject Diagnosis.*** The initial SZ diagnosis given to a proportion of neuroleptic naive subjects who are recruited into this study could be changed during the course of their admission. In order to maximize the number of microarray-analyzed samples from subjects who are correctly categorized as SZ, initial blood processing on all neuroleptic-naive patients who carry either a SZ diagnosis or a “rule-out” SZ diagnosis, following initial assessment and SCID diagnosis, is performed. This initial process includes the isolation and purification of the leukocytes, and storage of samples at -70°C, which ensures RNA stability for >6 months (Qiagen). The study team reviews subject’s notes and diagnosis twelve weeks after the subject’s admission. This time period will allow for a fuller set of notes to be created, and also for acquisition of patient notes and history from any other sources or institutions. Additionally, if a subject has been discharged, his discharge diagnosis and summary are present/available in the notes. Following this retrospective confirmation of subject’s diagnosis, 20 subjects were selected for GeneChip analysis.

***Neuroleptic-Treated Schizophrenic subjects.*** Twelve male neuroleptic-treated SZ subjects between the ages of 21-65 are completed in this study. Subjects will be recruited from a psychiatric center and community facilities. Male residents of the five facilities are screened. Exclusions at the chart level will include a diagnosis other than SZ. Patients are interviewed as to their interest in participating in the study and informed consent is obtained in accordance with IRB regulations. Records from previous hospitalizations are obtained and also used to confirm the schizophrenia diagnosis. Medical exclusions will be identical to those described for neuroleptic naive patient.

***Schizophrenia Diagnosis of Subjects.*** A psychiatric diagnostic and assessment interview is conducted by the study team using the SCID [5] in order to confirm the RPC chart diagnosis (neuroleptic-treated) or initial ER assessment (neuroleptic-naive) diagnosis for each subject. Patient records from previous treatment providers are obtained and also used to confirm the psychiatric diagnosis. Diagnostic interviews for the SCID will be conducted by the SCID trained members of the study team and the research nurse who is

also SCID trained and certified. For neuroleptic-naïve subjects, initial SCID diagnosis is retrospectively compared to subject's notes after 12 weeks, and only samples from subjects where there is agreement between the sources will be further processed for GeneChip analysis.

5           The Brief Psychiatric Rating Scale (BPRS), Clinical Global Impression (CGI), Mini-Mental State Exam (MMSE), Scale for the Assessment of Negative Symptoms (SANS) (Andreasen *et al.*, Br J Psychiatry 1989; Suppl (7), 49-58. 89), and Scale for the Assessment of Positive Symptoms (SAPS) (Andreasen *et al.*, Psychopathology 1995; 28: 7-17) are conducted by the study team or research nurse during the diagnostic and assessment  
10 interview. These scales are used to assist in the diagnostic process and to descriptively characterize the subjects.

**Drugs Abuse Screening.** Results from comprehensive urine screening for drugs of abuse including marijuana, cocaine, stimulants, barbiturates and heroin, performed at the time of admission or on the day of the study blood draw will be examined. Patients who  
15 refuse to be tested are excluded. Subjects are also questioned about cigarette smoking and number of cigarettes smoked per day.

**Control Subjects.** Fourteen male control subjects aged 21-65 are recruited from staff. The ages of the control subjects completed are defined by the patient sample and adjusted to maximize the similarity in ages between the groups. Controls complete a form  
20 (with the assistance of the study team) documenting that neither they nor their first degree relatives have a history of SZ, other psychotic disorders, mood disorders or of paranoid, schizoid, or schizotypal personality disorder. Current medication use and medical history are recorded. Medical exclusions are identical to those described for neuroleptic naïve patients.

25           **Blood Sample Collection, cRNA sSynthesis and Hybridization.** A fifteen ml blood sample is drawn from the antecubital vein by a phlebotomist or nurse. A CBC is performed on each blood sample. Blood is processed immediately to isolate and purify leukocytes, stored at 70°C and stored for further processing. Leukocytes are extracted from blood samples immediately following collection. The leukocytes are stable at -70°C  
30 (> 6 months, Qiagen), and storage at that temperature allows the retrospective

determination of which samples are to be hybridized to GeneChips, after a detailed analysis of all available patient history and a confirmed diagnosis of SZ. Samples chosen for RNA extraction are processed in duplicate, by splitting the extracted leukocyte samples and processing them identically thereafter. High density Affymetrix GeneChips and data analysis are described in Example 3.

**Quantitative RT-PCR.** Microarray analysis data are validated performing real-time RT-PCR on genes randomly chosen from those observed to be differentially regulated among leukocytes obtained from SZ patients and controls. Gene-specific primers are designed and employed for the SYBR Green PCR assay. Specifically, reverse transcribed cDNA is processed in duplicate from each patient RNA sample. Real-time PCR assays are then performed in triplicate for each cDNA sample. This replication should allow accurate confirmation and validation of the expression data from microarray analysis. This Example provides a leukocyte multigene expression signature that can classify leukocyte samples into SZ patient or control subject groups, which can be used to predict the class of unknown samples. A multigene expression signature that classifies leukocyte samples from both neuroleptic naive and medicated SZs is necessary because drug induced changes to gene expression patterns are a potentially confounding factor and may mask the disease specific signature for SZ. Recruitment of additional patients from all subject groups, and the inclusion of female subjects, ultimately will allow the power of the expression signatures to be calculated. This is facilitated by ongoing interactions with clinicians at all study sites, and should greatly facilitate the ultimate clinical application of the results.

This Example further establishes the ability to develop a database of specific leukocyte multigene expression signatures for other psychiatric disorders including bipolar disorder, schizoaffective disorder and major depression, which will in turn permit biological diagnosis of psychiatric patients. A longitudinal study, recruiting families with members at increased risk of developing SZ because of illness in other family members, is possible.

**EXAMPLE 7: ALZHEIMER'S DISEASE DIAGNOSIS WITH LEUKOCYTE MULTIGENE SIGNATURES**

The NINCDS-ADRDA and DSM-IV criteria are currently widely used for diagnosis  
5 of probable Alzheimer's disease (AD). These clinical criteria have a number of limitations,  
including lack of specificity and sensitivity in the diagnosis, and have an error rate of about  
10% even in academic research centers. Furthermore, diagnosis based on cognitive  
function can only be made post-symptomatically, at which time medications that may inhibit  
AD development or delay its progression will likely be ineffective. The imaging and  
10 biological marker diagnostic methods currently under development have additional  
drawbacks in terms of their need for highly specialized equipment, and specificity and  
sensitivity respectively, and thus may not be useful for early screening.

The present Example produces pilot data for development of a biological  
classification of AD patients, based on high-density microarray measurement of transcribed  
15 white blood cell (leukocyte) RNA. The rationale behind this proposal is based on two  
sources of data: 1) Current scientific literature, in which there is growing evidence that  
individuals with AD exhibit immune and other responses, that can be detected at the level  
of altered gene expression in circulating peripheral leukocytes. Quantitation of the mRNA  
transcripts in leukocytes of a number of individual genes has demonstrated associations  
20 between gene expression levels and the presence of AD. 2) Preliminary results from a  
microarray study by the PI, investigating gene expression changes in men with  
schizophrenia (Example 2, *supra*). Initial results from this expression study have been  
striking: supervised cluster analysis of peripheral leukocyte gene expression data, using  
transcript level measurements of thousands of genes from seven schizophrenic patients and  
25 five matched control subjects, resulted in a classification of all the subjects into their correct  
group. These results provide evidence to suggest that a surrogate tissue can be successfully  
employed for classification of a neuropsychiatric disease.

Utilizing a similar microarray strategy, this Example shows that individuals  
suffering from AD exhibit a conserved pattern of gene expression levels in their peripheral  
30 blood leukocytes, which is distinct from the pattern of expression in peripheral blood  
leukocytes from control subjects. This study provides a clinical assay that is minimally

invasive, and has the capacity to identify AD sufferers, and can also provide important pre-symptomatic and early stage diagnostic information.

### Background

Alzheimer's disease (AD) is the most common cause of degenerative dementia, representing about 65% of cases and affecting about four million Americans. Increased life expectancy, especially in the developed world has been accompanied by large increases in the AD rate, as its prevalence appears to double for every five years of age increase (Katzman *et al.*, (2001) In Iqbal, K., Sisodia, S.S., and Winblad, B. (eds), Alzheimer's Disease: Advances in Etiology, Pathogenesis and Therapeutics. John Wiley and Sons, Ltd. Chichester, England, pp. 11-21). AD is believed to have a long preclinical phase, followed by a mild cognitive impairment (MCI), characterized by mild memory loss. AD dementia then follows with progressive deficits across multiple cognitive domains, including attention, memory, verbal ability, visuospatial skill, problem solving and reasoning, and along with stroke may be the third most common cause of death in the U.S. (Ewbank *et al.*, Am J Public Health 1999; 89: 90-92). The growing economic and social costs of AD have made it a major public health issue, and prompted intensive study of its etiology and pathogenesis in order to facilitate development of preventative and therapeutic treatments.

Susceptibility to AD has a significant genetic component, and the discoveries of presenilin 1 and 2 (*PS1*, *PS2*), and amyloid precursor protein (*APP*) gene mutations that result in the familial forms of AD (early onset), have helped to elucidate the disease etiology Tandon *et al.*, Genome Biol. Reviews 2002; 3: 3014). However, familial AD accounts for only approximately 2% of all AD cases and although genetic risk factors for sporadic AD have been identified, for example the presence of the epsilon 4 allele of Apolipoprotein E (*APOE4*) (Farrer *et al.*, JAMA 1997; 278: 1349-56), many cases of AD do not carry the *APOE4* allele and have no known associated gene mutations. Therefore the remaining genetic effect in AD has yet to be identified, and likely involves several genes of small effect. There are major efforts underway to find genes that play a role in the development of the sporadic AD, through linkage analysis and association studies.

Several chromosome regions and many potential genes, including the TNF-alpha and the estrogen receptor alpha genes have been suggested as possible candidates, although there are some concerns with candidate gene association reproducibility.

5 Epidemiological studies have begun to show that early detection and treatment of AD may be associated with a more favorable outcome, involving both overall risk and also progression and severity of disease. A biological assay providing information that could help identify and classify AD and define susceptibility at an early stage, especially in high-risk families, could provide a great public health benefit. Such an assay would potentially allow for targeted treatment strategies to commence before the onset of many symptoms.  
10 Recent studies have also indicated the need for early and accurate differential diagnosis of AD from other dementias.

Diagnosis of AD is commonly performed using the NINCDS-ADRDA and DSM-IV criteria with direct patient assessment and interviews with family members. The criteria can provide a diagnosis of probable AD primarily based on cognitive function. Dementia  
15 severity can also be stratified according to the Mini-Mental State Examination (MMSE). Unfortunately, these diagnostic tools are inadequate for early diagnosis of abnormal changes in the brain that likely began long before cognitive impairment. Thus, even though highly skilled and experienced practitioners in a research center setting can achieve about 90% accuracy in patients meeting clinical criteria for dementia, several studies have  
20 documented the high levels of unrecognized dementia in the general community (Galasko *et al.*, Arch Neurol 1994; 51: 888-95). In addition, it has also been shown that the clinical criteria are unable to predict neuroimaging findings, suggesting that brain imaging is currently necessary in the diagnostic evaluation of dementia (Chui *et al.*, Neurology 1997; 49: 925-35). In order to improve the specificity of AD diagnosis and to develop pre-  
25 symptomatic and early stage diagnosis, neuroimaging (e.g., magnetic resonance imaging (MRI), positron emission tomography (PET), and single photon emission computed tomography (SPECT)) and biological marker detection techniques are under investigation in many studies. A few of these new methods and assays are described and the potential benefits and problems associated with each are discussed below.

Using fMRI, Bookheimer et al reported an increased magnitude of and extent of brain activation in the hippocampus, parietal and prefrontal cortex during a challenging memory test in subjects with the APOE4 allele, compared to those without an APOE4 allele, and concluded that during performance of a memory task, persons at risk of developing AD have preclinical compensatory increases in blood flow to those regions (Bookheimer *et al.*, N Eng J Med 2000; 343: 450-6). However, neuroimaging techniques are sophisticated and relatively expensive, and require a high degree of operator skill and interpretation. Implementation of these methodologies into the general clinical setting may prove difficult, and even in specialist centers evaluation may take several hours of patient and clinician time. Additionally, it is expected that an increase in current specificity and sensitivity of the techniques may require further development for practical use

Methods for the early detection, and diagnosis of AD by measurement of biological markers in CSF are currently under development and include measures of  $A\beta$ , tau and phosphorylated tau proteins, as they are intimately involved in the senile plaques and neurofibrillary tangles of AD. CSF levels of  $A\beta$  are decreased, and levels of tau and phosphorylated tau are increased in AD. However, their levels are variable and neither has the sensitivity and specificity for routine use or for screening CSF-derived measurements of biomarkers requires that patients to undergo a lumbar puncture. The requirement for a lumbar puncture, which is a fairly invasive procedure that causes some discomfort, would probably mean a CSF-based assay would be unsuitable for population screening and for future pre-symptomatic detection of AD.

In a large study of non-demented-, non-AD demented-, and possible or probable AD- subject groups, utilizing urine AD7C-NTP measurements, Munzar et al showed significant differences between the subject groups. There was however, considerable overlap in urinary AD7C-NTP levels between the groups, showing a lack of specificity (Munzar *et al.*, Neurol Clin Neurophysiol 2002; 2002: 2-8).

Measurements of  $A\beta_{42}$  in non-demented elderly subjects showed that, after 3 years, however, only those with upper quartile levels of  $A\beta_{42}$  were significantly more likely to



develop AD than those in the lowest quartile (Mayeux *et al.* Ann Neurol 1999; 46: 412-16). However, other studies have found inconsistent findings.

Serum Melanotransferrin (P97) was assayed in a group of possible and probable AD subjects, and healthy controls and significantly higher P97 was found in the possible/probable AD group, although there was overlap between the subject groups (Feldman *et al.*, J Alzheimers Dis 2001; 3: 507-16). In a similar study, Kim *et al.* measured serum P97 in controls, and AD and non-AD dementia subject groups and reported a significant difference between the AD group and the non-AD and normal control groups (also with the AD group elevated compared to the others), but no significant difference between the non-AD dementia group and the control group.  $\alpha$ -1 antichymotrypsin (ACT) levels were measured in serum from AD, VD, and healthy control subjects and were found to be significantly higher in the AD group than the other two groups, although ACT levels in the VD and control groups showed no difference. However, a lack of specificity of serum marker was inferred by the overlap between subject groups.

Tan *et al.* measured the CD45RO and CD45RA isoforms of CD45 on T-cells from AD, MCI, non-AD dementia, and age matched healthy control subject groups. They found significantly lowered CD45RA and increased CD45RO/CD45RA ratio in the AD patient group and in the MCI group, compared to the healthy control subjects. The non-AD dementia group did not differ significantly from the healthy control group, and there was considerable overlap in the CD45 isoform levels between the subject groups.

Currently the CSF assays for A $\beta$  and Tau have problems of specificity and sensitivity due to highly variable levels in CSF samples. Additionally, diagnostic assays requiring CSF samples are relatively invasive, would cause patient discomfort, may need a hospital setting and may require patient sedation. These factors may discourage use of CSF-based assays for population and pre-symptomatic screening, even if the assays themselves are improved. Although minimally invasive, the blood, blood-fraction and urine-based AD biomarker assays under development also have a relative lack of specificity.

Current antemortem AD diagnosis has variable accuracy and only produces a probable diagnosis. There is therefore a need for a sensitive and specific biological assay for AD diagnosis that can be performed using an accessible tissue, at relatively low cost, and without the requirement for sophisticated equipment at the site of sample collection.

- 5 This would allow for regular screening of pre-symptomatic subjects, and could also be used to assess the effectiveness of medications in the prevention and/or delay of symptoms.

To date, published microarray analyses of AD have focused on analysis of post mortem brain tissue to investigate the etiology of AD. Areas of the brain affected by the progression of the disease have been studied with exciting early results. Using cDNA  
10 microarrays, Hata *et al.* identified genes found to be differentially expressed between AD brain hippocampus and parietal cortex (but not differentially expressed in control subjects brain), and suggested that these genes may be regulated in response to neurofibrillary tangle-related destruction and are thus potential therapeutic targets (Biochem Biophys Res Comm 2001; 284: 310-16). Further dissection of the hippocampus was performed by  
15 Colangelo *et al.*, who employed Affymetrix arrays to identify gene expression specific to AD in the hippocampal cornu ammonis 1 (J Neurosci Res 2002; 70: 462), while Loring *et al.*, investigated expression in AD cingulate and amygdala brain sections (DNA Cell Biol. 2001; 20: 683). Strikingly similar results were reported from both studies, including the generalized depression in brain gene transcription, decreases in many known transcription  
20 factors, neurotrophic factors, and signaling elements involved in the synaptic pathway and also the up-regulation of genes involved in inflammatory, stress and immune and responses. These experiments have thus employed a global gene expression analysis to validate several theories of AD pathology and have identified pathways for future drug targeting.

Although microarray analysis of brain samples has and will provide important  
25 information on the etiology and pathogenesis of AD in brain tissue, it is obvious that use of brain samples from living patients for molecular diagnostic classification is not feasible. Thus, the development of any multigene expression-based classification of AD should focus on a tissue that is accessible. Peripheral blood samples are easily obtained and most significantly, it has previously been reported that patients with AD have altered levels of  
30 multiple gene products that are expressed in blood leukocytes.

In a recent study, Schipper *et al.* measured plasma levels of HO-1 protein in early sporadic AD, normal elderly control (NEC), normal younger control, age-associated cognitive decline (AACD), non-AD dementia, non-dementing neurologic illness and chronic medical disorder groups of subjects (Neurology 2000; 54: 1297-1304). The authors found that compared to the NEC group, the AD group had significantly lower HO-1 protein levels. Lymphocyte HO-1 mRNA levels were also measured for each subject, and were found to be significantly lower in AD relative to NEC, and levels were also found to be decreased compared to the AACD, non-AD dementia, non-dementing neurologic illness, and chronic medical condition groups. In addition, HO-1 mRNA levels were also lower in the AACD group compared to the NEC group suggesting a use for this transcript as a peripheral marker of both AD and age-associated cognitive decline. Transcript levels of the heat shock protein HSP-70 were also reported as a potential marker for AD. mRNA levels of HSP-70 in mononuclear blood cells were measured by Northern blot analysis, and although no correlation was observed between HSP-70 and aging, mRNA levels were found to be significantly lower in AD patients when compared to both VD patients and non-demented control subjects. In addition to the reports described above, further evidence for differential gene expression in AD leukocytes comes from multiple studies describing changes in the immune system in AD patients that result in abnormalities of peripheral blood lymphocytes, such as the multiple increases in circulating and in-vitro produced cytokines including CD4, CD25, and CD28 antigen, and decreases in CD7 and CD8, and the increase in T-lymphocyte IL-6 receptor 62. It therefore seems likely that for multiple genes, differential gene expression will be associated with the alteration in T-cell phenotype and dysfunctional immunity in AD.

Example 2, *supra*, reports that men with schizophrenia (SZ) exhibit a characteristic pattern of leukocyte gene expression, that differs from the gene expression pattern of healthy control subjects, and would thus be diagnostic for the disease. This study has generated very encouraging positive data by demonstrating that SZ patients exhibit a leukocyte gene expression pattern that differentiates them from controls. In addition, the seven schizophrenic patients analyzed in the study had medication profiles that were diverse and included several different classes of atypical and typical neuroleptic medications, providing some evidence to suggest that SZ subject classification from control subjects is

not directed by a specific medication profile. As reported below, these studies now include the analysis of additional subject numbers, including neuroleptic naive SZ subjects, to allow further development of a SZ leukocyte classifier. Data for comparison of multigene expression signatures between different psychiatric disorders are being generated. One major depression patient and two bipolar disorder patients, all of whom were receiving neuroleptics are recruited. Preliminary cluster analysis of leukocyte gene expression data showed a distinct separation of the bipolar and major depression subjects from SZ subjects, with an internal separation of bipolar from major depression. This data does show that the leukocyte expression signatures are disease specific and can be used to classify between different neuropsychiatric disorders.

Although it has been suggested that gene expression could be employed diagnostically for AD, using single markers, it seems clear that the measurement of multiple gene products as markers of AD provides considerably more detailed information for identification of the disease, and thus a more robust classifier than single (or dual) marker analysis. A recent investigation on SZ supports this assumption; Hakak *et al.*, showed a marked improvement in a brain expression classification of SZ subjects from control subjects when many brain markers were employed for analysis (n=35), compared to analysis of few markers (n=6), following linear discriminant analysis.

### Design and Methods

**Overview .** Microarray analysis measures the expression of leukocyte samples from 20 AD patients and 20 age-matched healthy control subjects. The study team obtains informed consent, and a 15 ml blood sample is collected from each subject prior to initial medication. Blood samples are processed to isolate and purify the leukocytes and the samples are stored prior to RNA purification, cRNA synthesis and GeneChip hybridization and scanning. Gene Expression data is analyzed by ANOVA testing, and by employing hierarchical clustering, and supervised learning algorithms.

**Subject groups.** Male AD patients and control subjects from all ethnic groups are recruited. There have been multiple reports in the literature of the ability of microarray analysis to accurately classify disease tissues even though micro-dissection was not performed to remove multiple non-disease cell types within the tissue. Additionally, a

recent report illustrated a classification of leukemia when whole blood was employed for initial RNA extraction (Armstrong *et al.*, Nat Genetics 2002; 30: 41-47). These papers suggest that the algorithms employed to determine signatures of gene expression are not confounded by either complex tissues (with only a sub-section containing the cells of interest), or inter-subject variation of genes in total peripheral blood. It is unlikely that expression variability due to ethnicity will mask an AD-specific leukocyte multigene expression signature.

**Recruitment of AD Patients.** AD subjects are recruited based on their initial evaluation and a diagnosis of probable AD. Candidate patients are approached and interviewed as to their interest in participating in the study. For patients interested in participating, informed consent is obtained. If possible, recruitment is limited to patients who have not yet received medication for AD, however medicated patients may be recruited into the study to ensure completion. Evidence from the SZ studies (Example 2, *supra*) suggest that neuroleptic medication does not primarily direct and/or mask leukocyte classifiers of disease. In addition, and if necessary for the AD research, subjects receiving a diverse range of medication treatments are recruited. This approach will decrease the likelihood that detected gene expression patterns are induced by a specific medication.

Patient's initial medical examination information is used to determine general health. Medical exclusion information for this study is ascertained by questioning of the subject and from family members and/or other collateral information. Medical exclusions include current or recent-infectious diseases, autoimmune diseases, proliferative disorders, and recent physical trauma or surgery, chronic immunosuppressant or anti-inflammatory medication use. Patients with CBC white cell counts outside of normal ranges are also excluded.

These selection and exclusion criteria have been designed to reduce the likelihood of detecting AD leukocyte gene expression patterns that differ from matched control subject gene expression patterns, but that arise not from the disease process but from other factors such as medication or the presence of an infectious agent.

**Male Control Subjects.** Twenty male control subjects are recruited from the staff and the local community. Subjects are in the age range of 65 and older. Control subject

age is defined by the patient sample as the ages of the control subjects are adjusted to meet the mean age of the patients, so as to maximize the similarity in ages between the groups. Thus control subject recruitment is initiated following the completion of AD subject recruitment. Control subjects are asked to complete a form documenting that neither they  
5 nor their first-degree relatives have a history of AD. Forms are also completed listing current medication use and medical history. Medical exclusions are identical to those described for AD patients above.

**Blood Sample Collection.** Fifteen ml Blood samples are drawn from the antecubital vein. A CBC is performed on each blood sample. Bloods are processed immediately to  
10 isolate and purify leukocytes, and stored for further processing.

**Quantitative RT-PCR.** Microarray analysis data are validated as described above by performing real-time RT-PCR on genes randomly chosen from those observed to be differentially regulated among leukocytes obtained from AD patients and controls. This  
15 Example results in the creation of a leukocyte multigene expression signature that can classify leukocyte samples into AD patient or control groups and can be used to predict the class of unknown samples (using a supervised learning approach). Recruitment of additional patient and control subjects and the inclusion of female subjects, allows the power of the expression signatures to be calculated. The data generated from this work permits investigation of the specificity of the multigene expression signatures by generating  
20 expression signature data for different forms of non-AD dementia. Longitudinal studies can be designed to generate multigene expression pattern data from pre-clinical subjects at risk of AD (through familial mutations or APOE4 alleles), and to investigate the feasibility of early diagnosis of AD utilizing multigene expression signature data.

Gene expression patterns that classify AD patients can be determined to be present  
25 in subjects prior to the onset of symptoms. It is thus possible to predict risk of AD from pre symptomatic subject's samples, potentially allowing for targeting of treatment to at-risk individuals.

A diagnosis of AD with improved specificity and sensitivity has multiple clinical uses, such as a diagnostic support to the clinician on initial presentation of the patient. Also  
30 of major importance for AD genetics research, multigene signatures could be employed to

assay members of AD pedigrees employed for genetic linkage studies. Affected members, having an accurate biological classification of diagnosis may help to avoid compounding errors in linkage studies.

5

**EXAMPLE 8: DETECTION OF GENETIC ALTERATIONS THROUGH GENE EXPRESSION IN SURROGATE SAMPLES**

Surrogate tissue can also be used to identify genetic defects or sequence alterations, such as mutations or polymorphisms, associated with, or resulting in, or contributing to, a physical state or susceptibility to a physical state. Genes/ESTs/sequences are shown to have altered expression in a surrogate tissue between the “disease” and “healthy” samples or subjects, and are potential candidates for having DNA mutations or alterations such as polymorphisms, that are related to the disease or physical state of interest.

The benefit of this objective is that it will necessitate sequencing of a smaller number of genes, to identify candidate “disease” genes, than currently used in other methods for discovering “disease” genes. Also, use of the present method for analysis of gene expression in surrogate tissues (*e.g.*, blood leukocytes) allows freedom of subject choice, and in the case of SZ, does not require access to postmortem brain tissue, or tumor biopsy tissue for the identification of susceptibility genes for cancer development.

This method can be employed for any physical state with a genetic component. Specific applications for SZ and prostate cancer are outlined below in Examples 8A and 8B. A list of candidates for further examination for prostate cancer is provided in Example 8B.

**Example 8A: Schizophrenia.**

Schizophrenia (SZ) is a complex disorder with a high heritability and approximately ten-fold increased risk in first-degree relatives. Genome scans are widely used in the search for SZ linkage regions, as prerequisite for identification and mutation screening of candidate SZ susceptibility genes. Studies to date possess a number of limitations, including lack of reproducible, strong linkage findings, and the large breadth of chromosomal areas identified, which can contain potentially hundreds of genes.

It is also believed that multiple genes of small or moderate effect may contribute to SZ susceptibility, and therefore need to be identified within the linkage regions. However, linkage studies have highlighted a number of chromosomal regions that may harbor genes that contribute to SZ. The difficult task is to identify susceptibility alleles among the large numbers of genes within these regions. Sequence analysis and association testing for all the genes within regions of linkage would be an overwhelming task and a more focused approach for candidate gene identification of is required. One embodiment of this method is designed, based on integration of linkage and gene expression data, for discovery and validation of SZ candidate genes..

Feasibility of this embodiment of the method was investigated using preliminary study gene expression measurements (from Example 2 above) of about 12,000 genes and ESTs from eight SZ patients and five control subjects (CS).

These preliminary study findings were very positive: 9774 genes and ESTs were mapped to the genome, and sorted and ranked by significance level of differential expression. In this particular example, genes were considered to be "expressed" if they had a GeneChip intensity of  $\geq 100$  intensity units (IU) (intensity values that were calculated through Affymetrix MAS 5.0 from a scaling factor of 100 for the data), and 1042 of the mapped, "expressed" genes were differentially expressed ( $p < .05$ ) between the eight SZ subjects and five healthy CS groups (note that use of an additional SZ subject has increased the number of genes found to be significantly differentially expressed from that described in Example 2) .

Mapped-gene expression data were then filtered using increasing GeneChip intensity thresholds, and the ten top ranking genes were each scored as mapping either to a region of SZ linkage (1), or to another genome region (0). The ten top ranked gene's scores were summed and recorded. When all mapped genes were included in the analysis (zero intensity filter) 2/10 genes fell within a region of linkage. A filter of increasing expression level stringency was applied in 20 IU increments, excluding genes for which less than two subject's IU values equaled or exceeded the IU threshold for that gene. Thirty complete, independent sets of randomized mapping data were generated and used to determine the frequency of random gene mapping to a linkage region.



For the real GeneChip expression data, when the IU cutoff reached 100, the number of linked genes climbed from 2/10 to 4/10. This was of interest because it was considered that GeneChip IU levels  $\geq 100$  indicated real gene expression, rather than background signal. As the IU filter threshold was further increased, the number of linkage regions  
5 genes within the top ten rose, reaching a maximum score of 6/10 at cutoff IU levels between 560 and 620. Scores of 6/10 between the 560 and 620 IU cutoffs were considered to be significantly higher than the background linkage region scores for the same IU cutoffs ( $p = .028$ ).

Since higher IU levels reflect increasing gene expression, the peak of SZ-linked  
10 region genes between the 560 and 620 IU cutoffs indicates the range of expression levels at which the noise of the system from in-specific differential gene expression has been filtered out. The remaining genes show disease-specific differential gene expression. Therefore, the overabundance or enrichment of top ranking genes that map to SZ linkage regions, seen at those cutoff levels, may provide the best candidate genes for DNA sequence analysis to  
15 search for gene and/or promoter, enhancer or splicing mutations.

At IU cutoffs over 620, the number of SZ-linkage region genes then fell back as the threshold was increased, dropping to a plateau of 2/10 at an IU cutoff of 720. The decreased representation of SZ-linked region genes in the top ten differentially expressed  
20 genes at IU cutoffs greater than 620 may be due to increasing representation of leukocyte-specific gene expression at these higher levels. This representation is likely due to, or reflective of, alterations in leukocyte expression of immune response mediator (IRS) and other genes, previously reported for SZ, and also due to the multigene expression patterns observed in the preliminary data for this study. Using this preliminary data, it was  
25 discovered that among the genes most significantly differentially expressed in leukocytes, between SZ and control subjects, there is a significant overrepresentation of genes from areas of reported linkage to SZ.

## Methods

Autosomal genes were sorted by increasing two tailed t-test significance level of  
30 differential expression ( $p$  value). For the purposes of this example genes/ESTs were

designated “expressed” if they had a GeneChip intensity of  $\geq 100$  intensity units (IU), and 1042 of the mapped, expressed genes were found to be differentially expressed ( $p < .05$ ) between the SZ and healthy CS groups.

Mapped-gene/EST expression data were then filtered using increasing GeneChip intensity thresholds, and the ten top ranking genes were each scored as mapping either to a region of SZ linkage (1), or to another genome region (0). The ten top ranked gene/EST’s scores were summed and recorded. When all autosomal mapped genes/ESTs were included in the analysis (zero intensity filter) 2/10 genes/ESTs fell within a region of linkage.

**Genome mapping.** Genes and ESTs represented as oligonucleotide probe-sets on the Affymetrix HU95A version 2 arrays, were mapped to their chromosomal sequence locations using the Ensembl Human Genome Browser (80%) and NCBI Human Genome Resource databases (20%). A total of 9774 genes and ESTs were mapped using these automated approaches, Genes without mapping data were excluded from the dataset.

A sample of genes and ESTs ( $n=81$ ) that had not been mapped by the automated approach, were mapped manually. There was no significant difference in the proportion of linkage area genes, when the manual and automated mapping approaches were compared ( $p=.689$ ), indicating that the automated gene mapping approach was not biased in the genes that it mapped.

### Results and Discussion

As illustrated in Figure 6, a filter of increasing expression level stringency was applied in 20 IU increments, excluding genes for which less than two subject’s IU values equaled or exceeded the IU threshold for that gene. Genes/ESTs that mapped to regions of linkage were assigned a score of 1. Genes/ESTs mapping to other areas of the genome were scored 0. The dataset was filtered with increasing stringency, using signal intensity cutoffs in 20 unit steps (*i.e.*,  $\geq 0, 20, 40, 60, \dots$ ). For each intensity cutoff, the number of genes/ESTs within the top 10 of all genes/ESTs, that map to regions of linkage were counted, and the y-axis values for the filled red circles each indicate the sum total of linked genes/ESTs within the top 10 genes/ESTs that were present, using the x-axis intensity cutoff level. The filled black circles indicate sum total of randomly occurring linkage areas

within the top ten gene/ESTs. Thirty complete, independent sets of randomized mapping data were generated and used to determine the frequency of random gene mapping to a linkage region.

This reasoning was based on the hypothesis that IU levels reflected increasing gene expression. Therefore, the peak of SZ-linked region genes between the 560 and 620 IU cutoffs indicates the range of expression levels at which the noise of the system from in-specific differential gene expression has been filtered out, leaving genes that show disease-specific differential gene expression. Accordingly, the overabundance or enrichment of top ranking genes that map to SZ linkage regions, seen at those cutoff levels, may provide the best candidate genes for DNA sequence analysis to search for gene and/or promoter and/or enhancer mutations or alterations.

A recent genome scan meta-analysis (GSMA) was used to select linkage regions for this preliminary analysis of gene expression data. (Lewis *et al.* Am. J. Hum. Genet. 2003;73:34–48). In this approach a rank-based meta-analysis was applied to autosomal data from 20 genome scans. Marker data was assigned to individual 30-cM bins and the bins were ranked by linkage scores, with weightings for sample sizes. Permutation testing was used to calculate the probabilities of the observed bin ranks, and 19 autosomal regions were identified where  $p < .05$  for weighted and/or unweighted analyses. Accordingly, in one embodiment, genes/ESTs identified in the present invention that map to the regions identified in the Lewis study are considered as being potentially SZ susceptibility loci.

The results demonstrate that that thirty three percent of the genes and ESTs were mapped to regions where linkage has been reported in a genome scan meta-analysis of 20 genome scans (Lewis *et al.*, Am. J. Hum. Genet. 73:34–48, 2003).

Prevalence of Significantly Differentially Expressed Genes is Enriched in Areas of Linkage to SZ. The total number of genes that map to SZ-linked areas were then compared with the total for genes that map to non SZ-linked areas of the genome. Interestingly, there was a 3.83 fold excess over expected values of significantly differentially expressed genes ( $p < .05$ ) mapped within SZ-linkage areas, compared to the total number of genes/ESTs that map to areas of SZ linkage. This enrichment finding further suggests that some of these

differentially expressed genes may be good candidates for being "disease or Susceptibility genes" for SZ.

*Linkage data is not a prerequisite or requirement for practice of the invented method.*

- 5 In many complex diseases, disorders and physical states, linkage data is not strong or reliable, or may not be available. One preferred embodiment of the present invention involves utilization of altered expression of surrogate tissue in a subject or subjects, for the identification of candidate sequences for testing by sequence analysis, without further selection based on whether genes/ESTs or nucleotide sequences lie at or near a region  
10 reported or considered to be linked to the disease, disorder or physical state being investigated.

#### **Example 8B- Prostate Cancer.**

- There is also substantial evidence of a significant hereditary component in  
15 susceptibility to- and of familial aggregation of- prostate cancer (PCa), with epidemiological studies having demonstrated a 2-3 fold increased risk of PCa amongst first-degree relatives of PCa patients (Whittemore et al, Am J Epidemiol. 1995, 141, 732-40). Although there are issues of heterogeneity, multiple studies have identified areas of linkage to the disease (Easton *et al.*, The Prostate, 57: 261-269, 2003; Janer *et al.*, The Prostate,  
20 57: 309-319, 2003; Brown *et al.*, Brit J. Cancer, 90: 510-514, 2004; Witte *et al.*, The Prostate, 57: 298-308, 2003.; Cunningham *et al.*, The Prostate, 57:335-346, 2003; Verhage *et al.* Familial Cancer, 2: 57-67, 2003). Several of the linkage regions have been identified and confirmed in independent populations. Regions identified to date include 1p36, 17q11, 19p13, 20q13 and Xq27-28. These results to date indicate the presence of  
25 multiple PCa susceptibility loci, and several individual genes within the regions have been identified as potential candidate PCa susceptibility alleles, these include RNA-SEL and ELAC2 (Carpten *et al.*, Nat Genet, 30: 181-184, 2002.; Tavtigian-SV., Nat Genet, 27:172-180, 2001).

The methods of the present invention were used to analyze expression data from men with PCa (n= 11) and male control subjects (n= 7). About 40% of the genes and expressed sequence tags (ESTs), represented on the HU95A version 2 GeneChip microarrays, used in this example were considered to be expressed (by the selected cutoff) in the leukocyte samples used, indicating that this accessible surrogate tissue is useful for the discovery and/or identification of candidate genes/ESTs by measurement of differential expression of genes/ESTs. About 599 genes were significantly differentially expressed between the PCa patient and control subject groups ( $p < .05$ ).

Mapping to the human genome was performed as described above.

## Results

***Differentially Expressed Genes Map to Areas of PCa Linkage.*** When the differentially expressed genes were ranked by significance level and mapped to the human genome as above, 55% of the 20 most significant genes were mapped close to regions of published replication-confirmed linkage to PCa. In order to control for any potential issues of PCa-linked genome regions possibly being over represented on the microarray, and to investigate the number of PCa linkage region genes that would be expected to appear in the top 20 by chance alone, repeated randomizations of the data were performed, and these were found to consistently result in about 20% of the top 20 genes mapping within regions of linkage to prostate cancer.

This strongly suggests to that the present invention will be useful for the rational discovery and/or detection and/or assay of potential candidate genes for mutation screening.

### Example 8C: Potential Candidate Genes or ESTs

Initial examination of pilot expression data and linkage regions has indicated a number of genes that are differentially expressed in PCa, and that map to regions of PCa linkage. Several are described below.

On candidate gene which was found to be significantly differentially expressed between PCa patients and healthy controls, and that maps to a region of linkage, is the potassium voltage-gated channel, shaker-related subfamily, beta member 2 (HKvbeta2.2)

gene, which was mapped to 1p36.3 (within 6cM of the positive LOD score region). This gene also was found to be upregulated in PCa subject group ( $p = .000041$ ) (Gibbs *et al.*, Am J Hum Genet, 64: 776-787, 1999). This gene is of additional interest because there is evidence of voltage-gated potassium ion channel protein overexpression in PCa specimens, and potassium channel blocking agents demonstrated growth inhibition in the LNCaP prostate tumor cell line (Abdul and Hoosein, Cancer Letters, 186: 99-105, 2002).

A second potassium channel gene that is significantly differentially expressed between PCa patients and healthy controls, and that maps to a region of linkage, is the Shaw type potassium voltage-gated channel Kv3.3 (KCNC3) gene. This gene was mapped to 19q13.3-q13.4, and was upregulated in PCa subject group ( $P = .0017$ ).

These findings indicate the utility of this invention for discovery, identification, detection, and evaluation of genes that are likely candidates for involvement in PCa susceptibility. Use of surrogate tissues and/or cells and/or organs (in PCa, peripheral blood leukocytes) permits of subject choice, and in the case of PCa, does not depend on the ability to acquire normal prostate or prostate tumor tissue, thus broadening the availability of samples by avoiding the requirement for a prostate biopsy.

#### **Example 8D: Proposed Study for Identification of Candidate Genes in Schizophrenia**

This proposed study is designed to test the feasibility of expression and linkage mapping as a method for discovering candidate genes within linkage regions, and to perform mutation analysis of the candidate genes. The longer term aims for this research are to extend this research to other psychiatric disorders and other diseases, disorders and physical states and all ethnicities.

**Study Design.** Blood leukocytes from twenty male and female SZ patients of non-Hispanic Caucasian ethnicity and twenty healthy control subjects between the ages of 21-65 will be collected over the two year period of this study. Affymetrix GeneChip microarray (*e.g.*, U133A) technology will be employed to measure global gene expression in the leukocyte samples, and significance testing will be conducted to identify genes differentially expressed between the two subject groups.

Genes and ESTs that are significantly differentially ( $p < .05$ ) expressed between the patient and control groups will be finely mapped to their genomic locations. The alignment settings will be stringent, only matches that have greater than about 98% identity or less than or more than 98% identity will be considered. In addition, significantly differentially expressed genes and ESTs that map within or near flanking markers of linkage to SZ will be cataloged and sorted by patient/control differential expression significance or level. Genes that map between or near the two markers of regions of linkage that has been will be included. Particular focus may be on areas previously shown or suggested to be linked to SZ, may include eg. 1q21-22, 6p22-24m, 6q21-22, 8p21m 10p11-15, 13q32, 22q11-13, and may also include 1q23.3-q31.1, 2p12-q22.1, 3p25.3-p22.1, 5q23.2-q34, 11q22.3-24.1, 6pter-p22.3, 2q22.1-q23.3, 1p13.3-q23.3, 8p22-p21.1, 6q15-q23.2, 6p22.3-p21.1, 10pter-p14, 14pter-q13.1, 15q21.3-q26.1, 16p13-q12.2, 17q21.33-q24.3, 18q22.1-qter, 20p12.3-p11, 22pter-q12.3 (Lewis et al., Am J Hum Genet. 2003;73(1):34-48).

Candidate genes cataloged as described above that have altered expression between the patient and control groups and that may also be included based on other factors eg. known or predicted to be expressed in the brain, will be selected. The candidate genes/ESTs or sequences, including 5' and 3' untranslated regions, controlling regions and all intron/exon boundaries will be sequenced in all patients and controls to determine mutations or sequence alterations.

Future studies such as evaluation using gene chips or other microarrays or other technologies, with more genes/ESTs or sequences (*e.g.*, U133 plus 2.0 from Affymetrix), may also include the investigation of genes/ESTs or sequences that have altered expression or eg. are differentially regulated between subjects with and without, and between different psychiatric disorders such as bipolar disorder and major depression and other disease, disorders or physical states.

### **Example 9: Refinement of Analysis to Detect Genetic Alterations**

The following methods can be used, (either individually, or in combinations of one or more additional methods), but are not a requirement for the practice of the invention.

One or more of these refinements can be used in conjunction with the initial invention to facilitate identification genetic defects by evaluating RNA expression in “surrogate” tissue.

**Refinement One.** Employment of the present method preferentially selects evaluation of genes or ESTs or other sequences of interest that are physically located within, near, or in the region of an area of linkage to the disease, disorder or physical state of interest. Such selection increases the likelihood that sequencing of a candidate loci meeting this criteria will yield a mutation or other genetic defect or alteration that is related to the disease, disorder or physical state of interest.

**Refinement Two.** The present method employs expression level-based exclusion filtering criteria to remove potentially spurious and/or non-relevant RNA expression data from data sets, following identification of candidates as described above. This technique can be applied by utilizing lower and upper expression level cutoffs. This is relevant to the present invention since it may be difficult to identify candidates among very low level expressors. Therefore, by using a “surrogate” or non-directly related biological sample tissue, any observed differential expression may be a product of non-physiological expression alterations. This rationale also applies in the case of high expressors, again because of the use of “surrogate” or non-directly related biological sample source. In this case, high expressors can be excluded as being of physiological importance in that sample or subject, unless, there is evidence the genes/ESTs/sequences under investigation have physiological relevance to the sample.

**Refinement Three.** The present method employs statistical testing to determine the significance of the differential expression between experimental groups being tested, *i.e.* “disease” and “healthy” or different physical state groups. This enables sorting or ranking of the genes/ESTs/sequences under investigation by the significance of their differential expression. Their relative significance can then be a factor in the selection of candidate genes/ESTs/sequences that are further selected for sequencing in search of genetic alterations or defects.



**Refinement Four.** A fourth refinement is the use of the size and/or degree of expression difference between experimental groups being tested, *i.e.*, between “disease” and “healthy” or physical state groups. The genes/ESTs/sequences under investigation can then be sorted and/or ranked by the size and/or degree of their differential expression, and  
5 their relative expression difference size will then be a factor in the selection of candidate genes/ESTs/sequences that are further selected for sequencing in search of genetic alterations or defects.

**Refinement Five.** The present invention also exploits expression information relating to the disease and/or condition and/or state under investigation. Information from  
10 studies or databases or other sources can be utilized as a method for filtering genes/ESTs/sequences to aid in the choice of candidates for further investigation by sequencing or other methods. Utilization of disease specific, tissue specific, or other specific expression information could also be a factor in deciding whether to exclude or include genes/ESTs/sequences from further analysis.

**Refinement Six.** Another refinement concerns use of expression information relating to organs, tissues, cells that are related to the disease or physical state under investigation. Information from studies or databases or other sources can be utilized as a  
15 method for filtering genes/ESTs/sequences to facilitate the selection of candidates for further investigation by sequencing or other methods.

This additional method is best applied by using it as a factor in the selection of candidates for further investigation, *i.e.*, assessing whether genes/ESTs/sequences under consideration are expressed or differentially expressed or have altered expression, in tissues associated with to the disease or physical state under investigation. Thus, for example, for schizophrenia, preference or priority for further investigation may be given to  
20 genes/ESTs/sequences that are expressed in the brain or central nervous system. Conversely these type of criteria could also be utilized in exclusion genes/ESTs/sequences from further analysis.

**Refinement Seven.** This invention exploits information concerning gene, loci, sequence and expression information relating to the disease, disorder or physical state under  
30 investigation. Information from studies or databases or other sources can be utilized as a

method for selecting genes/ESTs/sequences to measure/assay based on expression levels in order to assess samples for the potential presence of mutated and/or altered genes and/or sequences. For any disease, disorder or physical state under investigation, information from studies or databases or other sources is utilized to generate listings of

5 genes/ESTs/sequences as potential candidates. For example, where a previous study has named a gene as being of interest or shown association with, or has suggested biological or genetic expression or activity or function, in a disease, disorder or physical state, there is a rationale for its consideration as a candidate disease gene.

\* \* \*

10 The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

15 It is further to be understood that all values are approximate, and are provided for description.

Patents, patent applications, publications, product descriptions, and protocols are cited throughout this application, the disclosures of which are incorporated herein by reference in their entireties for all purposes.